

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 23:10:51 ; Search time 50.8403 Seconds
(without alignments)
3623.140 Million cell updates/sec

Title: US-09-508-967-1

Perfect score: 12100

Sequence: 1 MATSGSGGTODEDAKHVD.....VNKKKEIFEEERYPSIDWNI 2228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 8265679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA: *
2: /cgn2_6/ptodata/1/1aa/5_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4817	39.8	2182	1	US-08-487-826B-16
2	4802	39.7	3060	1	US-08-487-826B-14
3	3197.5	26.4	2710	1	US-08-568-459A-12
4	3197.5	26.4	2710	1	US-08-487-826B-12
5	3197.5	26.4	2710	2	US-09-210-288-12
6	3197.5	26.4	2710	2	US-10-153-273-12
7	1681.5	13.9	3542	2	US-10-087-013-2
8	1385	11.4	700	1	US-08-568-459A-10
9	1385	11.4	700	1	US-08-487-826B-10
10	1385	11.4	700	2	US-09-210-288-10
11	1385	11.4	700	2	US-10-153-273-10
12	702	5.8	921	1	US-08-568-459A-8
13	702	5.8	921	1	US-08-487-826B-8
14	702	5.8	921	2	US-09-210-288-8
15	702	5.8	921	2	US-10-153-273-8
16	445	3.7	311	2	US-10-087-013-10
17	439.5	3.6	407	2	US-10-087-013-8
18	422	3.5	294	2	US-10-087-013-7
19	418	3.5	1435	1	US-08-568-459A-4
20	418	3.5	1435	1	US-08-487-826B-4
21	418	3.5	1435	2	US-09-210-288-4
22	418	3.5	1435	2	US-10-153-273-4
23	386	3.2	308	2	US-10-087-013-11
24	379.5	3.1	362	1	US-08-568-459A-18
25	379.5	3.1	362	1	US-08-487-826B-18
26	379.5	3.1	362	2	US-09-210-288-18
27	379.5	3.1	362	2	US-10-153-273-18

28	375	3.1	351	2	US-10-087-013-9	Sequence 9, Appli
29	360.5	3.0	411	1	US-08-568-459A-19	Sequence 19, Appl
30	360.5	3.0	411	1	US-08-487-826B-31	Sequence 31, Appl
31	360.5	3.0	411	2	US-09-210-288-19	Sequence 19, Appl
32	360.5	3.0	411	2	US-10-153-273-19	Sequence 19, Appl
33	345.5	2.9	749	1	US-08-568-459A-6	Sequence 6, Appli
34	345.5	2.9	749	1	US-08-487-826B-6	Sequence 6, Appli
35	345.5	2.9	749	2	US-09-210-288-6	Sequence 6, Appli
36	345.5	2.9	749	2	US-10-153-273-6	Sequence 6, Appli
37	315	2.6	1115	1	US-08-568-459A-2	Sequence 2, Appli
38	315	2.6	1115	1	US-08-487-826B-2	Sequence 2, Appli
39	315	2.6	1115	2	US-09-210-288-2	Sequence 2, Appli
40	315	2.6	1115	2	US-10-153-273-2	Sequence 2, Appli
41	315	2.6	1115	6	5198347-6	Patent No. 5198347
42	311.5	2.6	1663	4	PCT-US93-07261-15	Sequence 16, Appl
43	288	2.4	1588	4	PCT-US93-07261-11	Sequence 11, Appl
44	272.5	2.3	2907	2	US-09-698-295-1	Sequence 1, Appli
45	272	2.2	10182	2	US-09-134-001C-3159	Sequence 3159, Ap

ALIGNMENTS

RESULT 1
US-08-487-826B-16
Sequence 16, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim T.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhuan
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knudde Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2182 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-487-826B-16
Query Match 39.8%, Score 4817, DB 1, Length 2182;

Best LocalSimilarity 45.9%: Pred. No. 5, 2e-311.
Matches 1096; Conservative 298; Mismatches 607; Indels 388; Gaps 93

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QY      4 SGGSG---GTOD-----EDAKHVLDIEFGQKVHE--VHEAKNVISELKSGSLAS-I 50
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Db     11 SGGSSSGGKKKQKOTSEYIYVSDAKDLIDRGEKEFYEEKVGNGAKYIEMAKGNLMTANGR
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QY     51 LGETAFTYKSMQTESKYTELIEANKRNCKDKGKNDVDRS-----VHEQAG 99
      |||||
Db     71 SSETASSIETCTLVKEYYERVVGDGRPHCRDARKADEVNRPSDTLGGQCTNRIIDSOQ 130
      |||||
QY     100 YDNKKMKCSNGMTCAPFRRLHLCNNKFPMMNSNDSSKAKHDLAEVCMARKYEGESIKTH 159
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      |||||
Db    131 GDNK-----GACAPYRLHLCDY---NLBSIDTSTTHKLLLEVCMAKTEGNSINH 181
      |||||
QY     160 YPKYDSKYPGSDPMMCMTLARSFADIGIIRGRDLYL--NKKKQNGETEREKLEQTL 217
      |||||
      |||||
Db    182 YLHQRTMEDSASQCTVLARSFADIGIVRGMDLYIGVDNKEKEQ-----RKLEQTL 235
      |||||
QY     218 KEIIFKIIH-DNLKXBAQKRYNGD--EDPNFYTLREDMWTANRETYGANTCSKELDNSSY 275
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      |||||
Db     236 KDIFPKIHDVWKTNGAQERYITDIAKGGDFPQLREDMWTSNREYWKALICHAPKANYF 295
      |||||
      |||||
QY     276 FRATNDPGGGGSQTHNKCRCODKDKAANGKPKAGAGDVITIPYTDYDYPQYLRMEEVA 335
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      |||||
Db     296 IKTACN-VGKG---TNGQCHC-----IGGD-----VPTFYDYPQLRMEEVA 335
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QY     336 EDFCRKKKKKLENLKQCRGKDKSDERYRYSRNGYDCEOTISRKGKVRMGKQCTDCCFAC 395
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Db     336 EDFCRKKKKKLENLQKGRDYEGN---LYCSNGYDCTKTIYKKGLVIGEHCTGNSVWC 392
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      |||||
QY     366 GSYEMWIDNQRQPFQKQ-KITKEISDGG-----RKRAVGGTIYE--GYEKSYEKL 447
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Db     393 RMYETWIDQKKEFLQKRRKYETELISGGSGSGKS PKTKGAARSSSSSDNGYESKRYKXL 452
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QY     448 KMDYGTUYAFLGLNNEKAKDITDGKINFEVNSGGGVVCGSGCGTSGASTDEMK 507
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Db     453 KEVGIQDVVKFLKILNKEGICQAPQVYG---NEKADN-----VDFTNEKYV 495
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QY     508 GTFYSEYVQPCPDGCVGHKGKGNOMERKTKVKKMRSKLYKPINGKVVLLSKLVKXDM 567
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Db     496 KTFSTETICEPCPWGLE-KGGPFW--VYKGDKTSASATKTYDPAINIDIPLYVDRSQ 552
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QY     568 MILKKNWEFCILTONSSDGSVGSVTTGASGGSSEKELYDEMKCYKANEVQKRVQGEV 627
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Db     553 QNILKYYKNFC-----EKGAPEGQIKN-----WQCY----- 580
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QY     628 BEDDDELKAGAGLCILPNPKKNKEVSEAK-----SQNHADIQKTFHDPFYVVAHMLKDS 683
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Db     581 ---DEHR-----PSSKNNNNVEGTMDFEQKQF--VKSIVFPMWVHMDLHDS 626
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QY     684 IHMRTKRLKSCI---SDGKTMCRNCGNKKKCDCEFEKVVQKETEWPRIKHDFEQDEGI-- 738
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Db     627 VEMKTE-LSKCINNTNGNTCERNKKCKTDCCGFCQVMEKQGEEMALIDHPEKQDIYQ 685
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QY     739 -----PEGYFTTLELILK---LQFLKEDTEENTENSIDAEAEELKHLQKILKE 786
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      |||||
Db     686 QKGLIVFSPYG---VLDDVLVKGNLNLQNIK-DVHGDY-----DDIKHKKL--LD 729
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      |||||
QY     787 NENNTLAVNAGTBQKTLMDKLNHLENDATKCC---DCPLREDSRGRSADPSDIFI 842
      |||||
      |||||
Db     730 BEDDAVAVVLGKQDNTI-DKLLQHEKEQAEQCKQOECEKKAQOESRGSATREDBRT 788
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QY     843 PRP-----BEKDDENEDDDDEVDDEETAETEGASLDTTTSLDV----- 885
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      |||||
Db     789 QCPADSAGVEBEEDDDDYDEDEDDDVQOEEBGE--RGTYTEVTEVAVEEVTQ 846
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      |||||
QY     886 -----CPIVKVLTKDNBSLDACSLKY--CGNNSSLGNRCVTPSGEPTTSDKNGALCY 938
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Db     847 BGWKPEDIYQK-LFEDDSGLKBAQGLKYGQGEKFPNNKCVTPSGVSTATSGKQALCY 905
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QY     939 PPRRRRLYIKYVMAKTKBSPQAGSSEASSTSGSTTPPDSK---EALKAFESALET 995
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Db	906	PPRRRLRYVGLSQWASR-----GDETTVESSSEATSAQSOSSEKLRPAFTAESAIET	955
Qy	996	FELMHAKREKKAUA-OEGAGHGLPRBEOSPXYDEPDXLKE-GKIPDGLRQMFYTLGD	1053
Db	960	FFLWHAKKEEKPPATDAGLQVSLPEPSPGSDPTDLOQGVIPDPLRQMFYTLAD	1019
Qy	1054	YRDLTFSGSNDTT-SVSGKTPSSSSNDMLKNI VLLASGSTEQEREKN-----KYEIKNFR	1108
Db	1020	YKOLLYGSGNDTPTTQKQTPSSSNDMLKNI VLEASSTGEKKNMQIQAKIKLILNGA	1079
Qy	1109	KCSTERSAPNLVSHR-OTWMENNGKTYIWHGNVCAJLSKDIKANGVEKK-PQKIENPENLW	1166
Db	1080	TSQVPVTKNSVKTPQOTWMENI AKOIMNAVCAJLYKENDAGTSAKIEONKOLKKALW	1139
Qy	1167	DEANKRKPPOYQYTNKYLDENSGTSFRITQYQASDNT--PRTLHFVYKPYTFRRFEE	1224
Db	1140	DEAKNTPPIEKYQYTNKYLBDESG-----AKSDNTIQPPLTKNFVEIPTFRRLHE	1190
Qy	1225	WGSFPCRERKRLKOIYVDCVKNVDGVRCSGDEACDSISTHYSIVPSPFCNGCCKHC	1284
Db	1191	WGSFPCRERAKRLQIYHCHMEDGGE-KQYSGDGEYEBEIPSKOYINVLQDLS-SSCAKPC	1248
Qy	1285	SSYKRYTERKKIEFHKOSNAYGQOKTD-----ATRNNGNPFDEKCKTLETWPDAA	1335
Db	1249	RLYTWJTEKKTEYERQKQKAYEQKSNYENBQKCKQTSNNNA--NEFSRTIQAASPTAA	1306
Qy	1336	KFLERLKNQPKTKNEY-GGDD-IDPEKSKTQHTHEYGCPKCFKTKNONGCGVSGL	1392
Db	1307	EFFQKL--GSGCKNNGYENGEDNKIDPKNDPKTEKHAHSCDPCBITGVKCKONGHC-VGSA	1363
Qy	1393	NG-NCDDPKSIDAKEIAMSSTTDVYMRVSDNTNFFE--GDDLKACQHANFVKIRK	1449
Db	1364	NGKCKKNKK-ITTAIDIKKTDPNQNIEMVYSDSTNFFELHG----CASSGIFKIRK	1417
Qy	1450	DVMKCGYCVGVDC--EQTNIERTDKEYI QIRALFKRWENFLBEDYNKINDKISHCIK	1507
Db	1418	DEWICANVCGVDITLKEKKIKNGGEGKXKITYMKELLKRWLEYLEDYNRIRKKIKLCTK	1477
Qy	1508	KGBSCKCINGCEKNSCKLEKWIIEKKIABMERIKKRFNDQIBNKQOPDYNVKSLIBELIPK	1567
Db	1478	KEDCCKCIKG-----CIEKVVQEKTEKMOKINDTYLEQYKND-----GNLTJNLEBQ	1525
Qy	1568	IAVVDQDNVTKLC-----VFENSGGCTLISNTQNNKNDKIDCMLKKLGVAKKCPGKPS	1623
Db	1526	FQYRTEFKNAITPCDGLDQFKTSCGLANSTDSQGNNDLVLCJLKLQKKISCKQHS	1585
Qy	1624	GEKQSDC-----KEP-----PLPDEBDONPEENTLEPPKCPPTTOPPEBKGE--TCG	1671
Db	1586	GQYQTPCNDNSLSKESITLVEDVDYERQN-EKVVQPKCPCPMKEPKKENDBEVGTG	1644
Qy	1672	NKEEKQBEKSESEPAKESGPAABEP--TASEBETLN-FBPPGTGPAAPSTPA	1728
Db	1645	GDEEKK--KVEDSVYBQKEEBAALAPESPPLTPEAKKEENVPKP-----	1690
Qy	1729	PPTDTPP-----LRQADEP-FDSIILQTTIPGVALLAGSIAFLFLKKTIRKASGN	1781
Db	1691	-----PPPKRRRIKTRVLDHPVIPALMSTTMSISIGFAFTFYLLKKTYSVGN	1744
Qy	1782	LEFQIQPKSDYDITPLKSNRYIPYVSDRYKGTIYIMEGSD-EDKYAFMSDTTYS	1840
Db	1745	LFQIQPKSYDITPLKSNRYIPYASDRKKGKTIYIMBEDSGDEKXAFMSDTTITS	1804
Qy	1841	SESEYBELINDIYVGSFKYKTLIEVVLBESGNNNTASGKNTBDFRNDIQD--GIP	1897
Db	1805	SESEYBELINDIYVGSFKYKTLIEVLEBS-----KRTIQNDIHNDIPSDIP	1853
Qy	1888	SS---KITDENKQKKEFISNMLQNPNDVDTYSGNSTYNTITTSRHHVNDNTN	1955
Db	1854	NSDTPPTITDEBNQKKDFISNMLQNTQNTEN-----ILHDVNDNTH	1898
Qy	1954	TTMSRDNNEKMLLPSTIHGVLGYGEEYSYV-----NMVN-----SMNDIP	1996
Db	1899	PTMSHNDQCPFTMSIHDRVLFGSEEBYNYMFSGNPNIIISDTYSMSDLTYSNHSFY	1958

[illegible]

RESULT 2
US-08-487-826B-14
; Sequence 14, Application US/08487826B
; Patent No. 5993827

Query Match	39.7%	Score 4802	DB 1	Length 3060
Best Local Similarity	36.2%	Pred. No. 8.6e-310		
Matches 1156	Conservative 277	Mismatches 631	Indels 1128	Gaps 83

0y 4 SGGSGGGQDDEADHGVLDPEFOKXVHDEHVEHAKNYSBELKGSJSLASJLIGFAFYKSMQT 63
0y 12 AAGDDIEDSAGHMFDRIGKOVYDVKYBEAERGGKQGRLS-----BAKFEKESDP 65
0y 64 ES-----KYTELEIANSKRNPK-----KDGKGNDDVRFVSVEQAGYNNKDKKC 107

Db	66	QTPEBPCDLDHKYHTNTVTTN--VINPCADRSVDVRPSDEVGCGCTNHRIDSSQGDNKC----	121
Qy	108	SNGMTCAFRRLLHCNKNFPMNNSNDSSKAXHDLAEVCAAKYEGESIKTHYPRYDSKY	167
Db	122	---ACAPYRLHVCODQLQEQIEPIKITTNT--HLLLVDCMAKAFEGSGSITODYPFYQATY	176
Qy	168	PGSDPMTMLARSPADIGDIIRGRDLATGNKKKKQKQKQKQKTEBREKLEQKLEIPKIDN	227
Db	177	GDSPSQICTMLARSPADIGDIVRGDVLGNPQLEK----ORQQLENNLLKTFIEKTYEK	231
Qy	228	LKDREAQRYVNGDDEDPNFYKLEREDMTANRETVGAMTCSKELDSSYFRACTNDTGOCP	287
Db	232	LNGBAA--RYG--NDPEFKLREDMTANRETVKALICNM--GNTYFTHCN---RG-	281
Qy	288	SQTHNKCRCXDKGKANNAKPRAGDGVTVTVPTFYDYVPOYLRFWEEMADPFCKKKKKLE	347
Db	282	ERTKGVCSCNDQ-----VPTYEDYVPOYLRFWEEMADEPCRKKNKKIK	325
Qy	348	NLEKQCRKXDSDEYRYCSRNGVYCEOTISKKGVRMBKSGTDCPFAGSYENMTDNOBK	407
Db	326	DVKNCRCRKXEDKDRYCSRNGVYCEKTKPRAIGKLRYSKQICSLCYACNPYDMTNQGE	385
Qy	408	QPDFKQ-KKYTEI-----SDGGKRKRAVAG--TTKEGYEKSFYEKLKNDYGTVDAF	458
Db	386	QPDFQKKRYDEIKYENGASGSGRQRADAGTTTNTDGYEKKRYDELNSEYATVQKF	445
Qy	459	LGLLNNEKACKDITD--GKINPFKEVNSGGVVGSGSGTSGASGTDENKGTFFRSEYC	516
Db	446	LEKLSNEEICTKYVDEEGTIDFKNVN-----SDTSGASGTNVESQGTFFRSKYC	496
Qy	517	QPCPDCCGVQ--HKG--NOWERKTKVVKQWRMSKLYKP--INGKNVLLKSLKVVKQMMI	569
Db	497	QPCPCGVKAYVNGGSSNMEWEKKN--GKCKSGKLEPRPDYKGTITTLTKSKGHD---	552
Qy	570	LKWKWKEKCLTQNSDGSVSVTTTGAAGSGNSEKKELYDEMVKCYKHNVEYOKVNVQGEVE	629
Db	553	IEBKLNKRCDBKNGDTINSGSGSGTGGSGGSGRQELVEBWKCYGDEYVVKGHDEDBE	612
Qy	630	DDBELKAGAGLCTLPNPKKXKVEBANSQNNHADIQKTFHDFPYTVVAHMLKDSIHWRTK	689
Db	613	DYEWKNAVAGGCLILKNQKKNKEBEGNTSEKPEDEIQKTFNFPFYVVAHMLKDSIHWK-X	671
Qy	690	RLKSGISDGTMKC--RNGCNKKRCDFEKVNVQKETEEMKPIKDNFTQSGIDREGYFTTLE	748
Db	672	KLQRCLQNGRIKIGGNMKNANDCECFKRWITQKQDEMKIYQHFQTQIYKGRGSDNTAE	731
Qy	749	LI-----LKLQFLKED---TEBNTENSIDAEAEELKHLQKILKLENNENLAV	793
Db	732	LIPRHDVVLQYNIQEBFLKGSDESDASEKSEKENSIDAEAEELKHLREIISEDVNOEAS	791
Qy	794	VNAG--TEQKTLMDKLIHNLMDATYCKDCSPRPEBK-----	828
Db	792	VGGVTEQKINMDKLIHNEKDEADLCLEIHDEBEKKEKGDNECIEBGENFRYNPCSGE	851
Qy	829	-----	828
Db	852	SGNKRYPLANKVAYQVNHKAKTQLASAGSALRGLDLSLAQFKNGRNGSTLKGQICIKN	911
Qy	829	-----SHGRSADPS-----PDIFIP-----	843
Db	912	ENYSNDSRSGNGGPGCTGKQDGHGVBRMIGTEWSNIEGKQTSYKVNFLPRRREHCTS	971
Qy	844	-----	843
Db	972	LENIDVGSVTNKDKASHSLGADVOLAAKTDAAEIIRKYQDNNIQLTDPLOQKQDEAMCR	1033
Qy	844	-----	843
Db	1032	AVRYSFADLGLIIRGRDWMEDKSDTMEHTLLIYFKNIKXKHQISIKONPKYTQDSKCP	1099
Qy	844	-----	843

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Db 1092 AYKKLRADWBEANRHOVRANKCATKGIICPMFVDYIIPQRLRMTEMAEYCKAOSQE 1151
QY 844 ----- 843
Db 1152 YDKLKICADCMKSGDKCTQGDVDCGCKAACDCKYKEIEKMNQWMIKIDKYNLYLQ 1211
QY 844 ----- 843
Db 1212 AKTTSTNPGRTVLGDDDDPDYQOMVFLTPRHKASIAAEVLVRAAGSPTEIAAAPTTPY 1271
QY 844 ----- 843
Db 1272 STAAGYIHQEIYGGCGEQOTQCEKKGATSTTKENKEYTFKQPPPEYATACDCINRS 1331
QY 844 ----- 850
Db 1332 QTEBPKKKEBNVESACKIVKILBGNRTTVEGCPKESYPMDCCKANIDISHGACMP 1391
QY 851 ----- 863
Db 1392 PRQKLCUYIAHESQENIKTDNLKDAFIKTAABTFLSQYKSKNDEBAKILDRGL 1451
QY 864 ----- 875
Db 1452 IPSQFLRSMMTTFCGYRDI CLANTDISKQNDVAAKAKKIKGFPSKSGSKSPSGLSRQEW 1511
QY 876 ----- 879
Db 1512 KTNGEIKKGMCLTKYVTDTDNKRKIKNDYSYDKVNOGNGNSLEBPAKQFLRM 1571
QY 880 ----- 879
Db 1572 IEMGEFCAERQKENIIKDACEINSTQCCNDAGHCNQAQAYEYENKKKEPSQOT 1631
QY 880 ----- 879
Db 1632 NNFLKANVQODPEYKGEYKQVQPTQGNFYLLQKCDNCKSCMDGNLSVSPKKEPF 1691
QY 880 ----- 903
Db 1692 GKVAHKEYEKDCYCGKGVPSIPPPPPYQOPQPEAPATVTDVCSIV-KTLFMDTNFSDA 1750
QY 904 CSLKYGNNRSLGMRV---TPSGEPTT---SSDKNGAICVPPRRRLYIKIYDWMATKT 957
Db 1751 CGLKTY-GKTAPSSWKCIPSDTSGAGATTGSGSGSGSICIPRRRRRYVYGLOQEMATL 1809
QY 958 BSPQASGSASSTGPTTTPDSKALLKAFVESAAIEFPLMHRKKEBKAAOAGAGHG 1017
Db 1810 --PQEBGAAPSHSRA-----DRLRNHFIOSAIETFFLMDRYKEKKPQG-DGSGQA 1858
QY 1018 LPRVEE--GSPPEYDEBK-LKEGKIPDGFLRMFYLLDYYRDLIFSGSNDTTSYSKOTPS 1074
Db 1859 LSQLSTYSDBEDPDYKLGKGIIPDFPLRMFTLDDYRDLVHGN--TSDSGNTNG 1916
QY 1075 SSSNDLKNI VLLASSTBOERKMKMKKEI--KMRKSTESASANLVSHPTWMEANGK 1132
Db 1917 SNNN--NIVLEASGNKEDMKIOEKIRQILPKNGTPLVPSK--AQTPDKMNEBAE 1970
QY 1133 YTHHMMVCAIT-----SKDIAKGVKKPKQKINPENLME-----ANKK-----BKP 1175
Db 1971 SIKWMICCALYTEKKNPDTSSARGD--NKLEKDEVEYKFPFGSTADKIGASTTGTGYK 2027
QY 1176 POYQYTNVLDENSGTSPRTTQTOASSDNTPTTLTHFVAKPTYFPMFEBEGSPCEKKEK 1235
Db 2028 TOYDIEKYKLEDTSG-----AKTPSASDTP-LLSDFVLPRPYFLYLBEGWGNFCCKKKH 2081
QY 1236 RLKQIKVDCKVENGVG-----RCSGDGACDISITHDYSTVSPFNCPCGKHCSY 1287
Db 2082 KLAQIKHECKVENEGSGSRGIGITRQYSGDGEACBEMLPKNGGTVPDLLEKPSACAPCSSY 2141
QY 1288 RMYIRPKKIEFKHQSNAVGOQKTDAIRNNGNTFDEFCCTLETTWDAKFLERLNGQCK 1347
Db 2142 RWMIESKGKEFKQEKAYEQOK-DKCVNGSNKHNGFCBTITLTSKADFLKTL--GPCK 2198

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QY 1348 TNKEYGDDIDFEKDSKTFQHTTEYCGPCPYFKTNCQNGCVSGLNGCQGDSDAKKEI 1407
Db 2199 PNNVEGKTIPD---DDKTFKHKTCDPCLKFSVAVCKDEBD-NSKGTDCRRKNSIDAKTDI 2254
QY 1408 AXGRSSTTDVVMRSDNDTTFEGDDLKDA COHANIIFKGI RKOVMWKGCVGVGICBOTN 1467
Db 2255 ENGVDSIV-LBMRVASKSGFNGDGLNACRGAGIEGIRKIDMKRANVCYGVCKPEN 2313
QY 1468 INERTDKEYIOTRALFKRWENFLBDYNKINDKISHCIRKSGSKCINGCKNSKLEK 1527
Db 2314 VNGSAKXKHIIQIRALVYRWVEYFEDYNNKIKHISRIKNGEISPCI---KN--CYEK 2367
QY 1528 WIEKIAWENIKKRPNDOYBNKOQPRYNKSLBELIPKIAVNDODNYTKLCVFENSK 1587
Db 2368 WVDQKRKEMKEITERFQDYQNDNSDDNVRSPLETILPQTTDANAUKYIKSKFNSNC 2427
QY 1588 GCTLISNTO--NNKENDAIQMLKCLGVKAKNCPG--PSGEKQSDCKEPPPLPDE--- 1639
Db 2428 GCSASANEONKNGEYKDAIDCMLEKLDKDIGECKKHQTSBTECSOTPPQPTLEDTLD 2487
QY 1640 ---EDQNPBENTLEPPPCFPT--TOPPEKGETCGNKKEKDEKKESEBPAKESGP 1694
Db 2488 DDITEBAKKNM--PICEVVLTKAQEDBG--C-----VPAENSBEPAATDSGK 2535
QY 1695 AAEEPAFTASEETETNPPPEPGTGPAPSTPAP---PIPDTPPLRPOADEPFDSTIL 1751
Db 2536 ETPEQTPVLKPEEBAVPEPPP-----PPOEKAPAPIPOQPPPTTOLLDNHVTAL 2589
QY 1752 QT-TIPPGVALGSIAPFLKXKTKASVGNLFOILQIPKSDYDIPFLKSANRYIPVSD 1810
Db 2590 VTSTLANSVGI GRAFTFYLLKKTIKSSVGNLFOILOIPASDYDIPFLKSANRYIPTSG 2649
QY 1811 RYKGGTYIYMEGDSDEBKYAFMSDTPDVTSSESEYEBELINDIYVPSPKYKTLIEVLE 1870
Db 2650 KYRGKRYIYLBGDSGDS--GYTHYSDITSESEYEBEMDINDIYVPSPKYKTLIEVLE 2708
QY 1871 P-----SGNNTTASGKATPSDTRANDIONDGI PSKITDNEMWOLKEPISN 1916
Db 2709 PSGNNTTASGNNTTASGNNTTASGKNTPSDONDIONDGI PSKITDNEMWOLKEPISQ 2768
QY 1917 MLQNOPDVPNDYNSGNSSTNTNITTSRHVNDNTTMSRDMMEENLPLSIHDGNYL 1976
Db 2769 YLQSEEPNTEPN-----MLGIVDNNHTFTSHANVEEKFPMISHDRNLF 2813
QY 1977 SGEESYVNV-----NMVN-----SMNDIPINRDNVYSGIDLINDLSLGGKPI 2019
Db 2814 SGEESYVNDMFNSGNPINISDSTNSMDSLTGNNHSPYNDKNDLYSGIDLINDALSGNH-I 2872
QY 2020 DIYDEVLRKKNELFGTE-NTKRTSTQNVAAITNSDPIHNLLELFHKWLDHRMCEKWK 2078
Db 2873 DIYEMLRKKNELFGTKHTKHTNTYNAKPARDDPTVQINLFHKWLDHRMCEKWK 2932
QY 2079 NKEDIILKKEEMKENINNSGKTYNSDNKSHHVLNTDVSIQIDMDNPTKKEITNMD 2138
Db 2933 NNHERLPRKLELM--ENETHSGDI--NSGIPSGHVLNTDVSIQIDMDNPTKKEITNMD 2988
QY 2139 TNQDKSTMDITLDDLEKXNDPYDYDFEYDDI IYHDVVEKSSMDIYVDAHNVTSNNMDV 2198
Db 2989 TNPDKSTMDITLDDLEKXNEBYDYDFEYDDI IYHDVVEKSSMDIYVDAHNVTTNNMDV 3048
QY 2199 PTKKHIEKNIVN 2210
Db 3049 PTKKHIEKNIVN 3060

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RESULT 3

US-08-568-459A-12

; Sequence 12, Application US/08568459A

; Patent No. 5849306

; GENERAL INFORMATION:

; APPLICANT: Sim, Kim L.

; APPLICANT: Chitnis, Chetan


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QY 864 -----DEETAKE-----TTBGS----- 875
Db 1454 IPSQFLRSMYTFGDYDICIINTDISKQNDVAKAKXIGKFKSGSKSPSGLSROBWW 1513
QY 876 -----ATDT----- 879
Db 1514 KTNGBELWKMALTKYVTDITDKRKIKNDYSYDKYNQSGNPSLEBFAKQFLRMW 1573
QY 880 ----- 879
Db 1574 IEMGEFCAERQKXENIIKQACNEINSTQGCNDAKHRCNQAQYQVEVENKXKKEFSQOT 1633
QY 880 ----- 879
Db 1634 NNFLKANKVQPODEYKGYEKDQVPIQGNBYLLQCKDNKNCSCMDGNVLSVSPKPKPF 1693
QY 880 -----TSLVLCPIVGVVLTKDMBSIQDA 903
Db 1694 GKVAHKYPEKCDYQCKHVPSPIPPPPPVQPOPEAPVTVVCSIV-KTLFKDITNNFSDA 1752
QY 904 CSLKYGNNSRLGNRCV---TPSGEPTT---SSDKNGAICVPPRRRLYIKKIYDMATKT 957
Db 1753 GGLKY-GKTAPSSMKCIPSDTKSGAGATTGSGSGSGSICIPRRRLYVGLQDMATL 1811
QY 958 ESPQASGEASSTSGTTPPDSKEALLKAFVESAIIETFLMHRKYERKKAQAQEGAGHG 1017
Db 1812 --POEGGAAPSHSRA-----DILRNAFIQSAAIETFFLMHRYKEKKEKQDQ-DGSOQA 1860
QY 1018 LPRVBE--GSPBYPEDEK-LKEGKIPOGLFQMPFTLDGYDIIIFSSGNDTYSKDPSS 1074
Db 1861 LSQLSTYSDBEDPDLQNGKIPDFLRLMFTLDGYDILVHGGA--TSSGNTNG 1918
QY 1075 SSNDLKNIIVLLASGSTEQERKNNKYKEI--KNFRKCTERSAPNLVSHQPTWENNGK 1132
Db 1919 SNNN---NIVLEASGNKEDMKIQKIEQILPKNGGTFLVKKSS---AQPTDKMNHAE 1972
QY 1133 YIMHGMVCAIT---SKDKIAKGYEKKQKIENTENLMD-----ANKK-----PKP 1175
Db 1973 SIMKMICALITYTEKNPDTARSARDE--NKIEKDEVEYEKFGSTADHGTASTPTGTYYK 2029
QY 1176 POYQTNKLDENSGTSPRTQTOASNDTPTTLTHFKRPTTYPFPMESGFCREKXK 1235
Db 2030 TQYDEKVKLEDTSG-----AKTPASSDTP-LISDFVLARPYEFLYLEWQGNFCFKKXK 2083
QY 1236 RLKQKIVNCKYENGQV-----RCGDEGACDSISTHDYSYVPSFNCGCGKHCSSY 1287
Db 2084 KLAQIKHECKYBENGSGSRGGITQYSGDGEACHEMLPKNDGYVPLDEKXSCAKGCSY 2143
QY 1288 RKMIERKKIEPHKQSNAYGQOKTDTATRNNGTFFDEKFKTLETWPAKFLERLKNPCK 1347
Db 2144 RKMIESKKEFEKQKAYEQK-DKCVNGSNKHGNGFCETLITSSKADFLKTL--GPCK 2200
QY 1348 TNKEVGSDIDPEKSKTFQHTYEGYCPKFTNQNQNGCVSGSLNGCDDQSDAKEI 1407
Db 2201 PNNVSGKTIPTD---DDKTFKHTKDDPCLKFSVNCXKDECD-NSKGTCCRNKNSIDATDI 2256
QY 1408 AKMRSSITDVVWRVSDNTNTPFEGDDLKQACOHANIPIKGIARDVYKCGVGVDCIQTN 1467
Db 2257 ENGVDSTV-LEMRVADSKSGNGDGLNACGAGAIIFSGIKRDEKKNVCGYVCKREN 2315
QY 1468 INERTDGKEYIQIRALFRKVENFLDYNNKINDKISHCIIKKGESKJINGEKNSKLEK 1527
Db 2316 VNGEAKGHIIQIRALVYKRWVEYFEDYNYKIKHKTSHRIKNGEISPTI---KN---CYEK 2369
QY 1528 WIEKIIAEMENIKGFNPQYENKQDPDVNVKSIIEELIPKIAVVDQDNVILKCYFENSK 1587
Db 2370 WVDQRRKKEKELITERFKQYKXNDSDDNVRSFLETLIPQITDAKAKKVKILXSFNGSC 2429
QY 1588 GCTLSINTQ--NNKENDAIQMLKTLGVYAKKCPK---PSGKQSDCKEPPPLDE--- 1639
Db 2430 GCSAANBQNKNGEKYDAIDCMKTLKDKIGSECKKHQTSPTESDTPPQPTLEDFLTD 2489
QY 1640 ---EDQNPBENTLEBPKFCPT--TQPEBEKGETCGNKEKXDEKESSEBPAKESGP 1694

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Db 2490 DDIETESAKNNM--PITCENVLTKAQOEDGG--C-----VRAENSEEPAADSGK 2537
QY 1695 AAEPAAPTAESBETETNFPPEPGTGPAPSTPAP---PPDTPPLRPQADEPPTSTIL 1751
Db 2538 ETPEQTPVLKEBEAVDEPPPP-----PQEKAPAPAPQPPPTPTQLDNPVLTAL 2591
QY 1752 QT-TTFPGVALAGSIAFLFK 1772
Db 2592 VTSTLMSVIGIGPATFTFYFLK 2613

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RESULT 4
US-08-487-826B-12
; Sequence 12, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnie, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th floor
; City: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 415
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelien, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-0176
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
US-08-487-826B-12

Query Match 26.4%; Score 3197.5; DB 1; Length 2710;
Best Local Similarity 30.6%; Pred. No. 3.9e-203;
Matches 834; Conservative 244; Mismatches 569; Indels 1075; Gaps 74;

QY 4 SGGSGGTODEBARKVLDLDFQGVHDEYHGEAKVNVSELKSGLSLASTIGETAFYVKSQT 63
Db 14 AAGGDIDIESAKMPRIGKDVYDKVEAKERKGLQGLS-----EAKFERNSDP 67
QY 64 ES-----KYTELEANSKRNPCK-----KDGKNDVDRFSVYEQAYDNKKKCK 107
Db 68 QTPEDPCDLHKKYTNVTTN-VINPCADRSDVRFSDEYGGCGCTINRIKDSGGGNKG--- 123

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QY 108 SNGMTCAPRRLHLCKNKPMMNNSDSSKAGHDLAECMAKYEGESIKTHPYRDSKY 167
 Db 124 -----ACAPYRLHVCDDQLEQIBPIKINT--HNLLVDCMAKEGSGITQDYPYQATY 178
 QY 168 PGSPBPCMTLARSFADIGDIIIRGDLYLGNKKKKQNGKETEREKLEBOKLKEIFKIHON 227
 Db 179 GDSFSQICMTMLARSFADIGDIYRGDLYLGNPOEIK-----QROOLENNLTTIRGKIYEK 233
 QY 228 LKJDEAKQRYNGDEBPNFYKLREBMMTANRETMWAMTCSKELDNSSYFRATCNDTQGP 287
 Db 234 LMGDA--RYG--NDPEFFKLREBMMTANRETMWALITCNAM--GNTYFHAFCN--RG- 283
 QY 288 SOTNKKCRCDXKDGANAGKPRAGDGYIVPTPYDYVQYLWFEEMADECRKKKKKLE 347
 Db 284 BRTGYCCKCNDQ-----VPTYPDYVQYLWFEEMADECRKKKKK 327
 QY 348 NLEKQCRKDXSDEYRYCSRNGYDCEQITSRKGVKMGKGTDCFPAGSYENMIDNRK 407
 Db 328 DVKENCRCXKDEKORYSRNGYDCEKTKRAIGKLRGKQICISCLYACNPYVDMINQKE 387
 QY 408 QEDKO--KRYTKEI-----SDGGKRRKAVG--TTKEGYEKSFEYELKNDGYVDAF 458
 Db 388 QFDKQKKYDEIKKYENGASGSQRKQDAGGTTTNTDYEKKEPYDELNKSERYVDKF 447
 QY 459 LGLANNEKACHDITD--GKINFEKVNAGGVGGSGTSGASTNDEKGTFRSEYEC 516
 Db 448 LEKSNBEICTKRVDEBEGTIDFKNVN-----SDTSGASTNDESGTFRSEYEC 498
 QY 517 QPCPDCCVQ--HKQ--NOWERKTKVKKRWSKLYKP--INGKVVLLKSLKVVKDMTI 569
 Db 499 QPCYCGVYKVNAGSSNMEEEKNN--GCKSGKLYEPKPDKEGTTITLKSGKGDH-- 554
 QY 570 LKKRMKECLTONSDSGSVVTTGASGSEKKELYDEMKCYKHEVQVKNVQGEVEE 629
 Db 555 IEEKLNKFCDEKNDJTINSGGSGGSGNSGRQLEEMKCYKGBEVVVYGHDEDEE 614
 QY 630 DDELKAGAGLCTILPNPKNKEVSEAKSONNHADIOKTFHDFYVVAHMLKDSIHWRTK 689
 Db 615 DYENKARAGGLCTILKQKKNKEBEGNTSEKPEDEIOKTFNPFYVVAHMLKDSIHWK-K 673
 QY 690 RLKSCISDGKTMKC--RNGCNKKDCFEKRVKOKETEMWPKIDHFKTOEGIRGEYVFTTLE 748
 Db 674 KLGQCLQNGNRKIKCGNNKCNNDCECFKRWITQKDEMGKIVQHFQTIQIKRGSGSDMTAE 733
 QY 749 LI-----LKLQFLKED-----TRENTENSIDAEBAEFLKHLQKILKEBNNILAV 793
 Db 734 LIPPDHDIYVLOYNQOEFLKGBSDASEKSENSIDAEBAELKHLREIIESEDNQDAS 793
 QY 794 VNAG--TEOKTLMIDLNLHNLDAATKCDKCPLEBDK----- 828
 Db 794 VGGGVTEOKNIMDKLNLTEKDBADLCLEIHEDBEBEKKGDNCEIBEGENFRYNPCSGE 853
 QY 829 ----- 828
 Db 854 SGNKRYPLANKVAYOMHHRKAKTOLASRAGSALRGDISLAQFKNGRNGSTLKQOICKIN 913
 QY 829 -----SRGRADRS-----PDFIFP----- 843
 Db 914 ENYSNDSRNGSGPCTGKDGHHGVRMRIGTEMWNIIEGKQTSYKKNVFLPRRBHMTSN 973
 QY 844 ----- 843
 Db 974 LBNIDVGSVTKNDKASHSLDLVDVQLAAKTDAAEIIKRYKQNMNQLTDPIDQKXQOAMCR 1033
 QY 844 ----- 843
 Db 1034 AVRSYFADLGDIIIRGDMWDEBDSKSTDMETRLITVFNKIKKHHGIXONPKYTGDESKP 1093
 QY 844 ----- 843
 Db 1094 AYKKLRADWMEANRHOVRANKKATKGIICGMPVDYIIPQRLMWTBMAEWCKAOSQE 1153
 QY 844 ----- 843

Db 1154 YDKLKIKIADOMSKXGDKCTQGDVDCCKRAACDKYEBIEKNNEQWRKISDKYNLLYLQ 1213
 QY 844 ----- 843
 Db 1214 AKTSTNPGRTVLGDDDDPYQQWVFLPLPIHKASIAARVLVKRAGSPTEIAAAPTTPY 1273
 QY 844 ----- 843
 Db 1274 STAGYIHOEIGYGCQEOQOFCEKKGATSTSTTKENKETYFKQPREVATACDINRS 1333
 QY 844 -----RPEEKED----- 850
 Db 1334 QTEPFPKKEBENVESACKIVEKILEGNKGRITTVGECNPEYSYPMDCNNIDISHGACMP 1393
 QY 851 -----DEN-----EDDEDEVRD--- 863
 Db 1394 PRROKCLLYIABESQENIKTDNDLADAFIKTAABTFLSWOYKSKKNSEAKILDRGL 1453
 QY 864 -----DEBFAKE-----TTGS----- 875
 Db 1454 IPSQPLASMTYTBEDYDCLANDTISKQNDVAKAKKIGKFKFSKDSKSPSGLSRQEW 1513
 QY 876 -----ATDT----- 879
 Db 1514 KTNGBEIKMGMLCALTKYVTDITDNKRIKNDYSYDVKNQSONGNPSLEFAKQPLRWM 1573
 QY 880 ----- 879
 Db 1574 IEMGEFCAEROKKENIIKDACEINSTOOCNDAKHRCNOACRAYOEVENKKEFSGOT 1633
 QY 880 ----- 879
 Db 1634 NMFYKANVQPOPEYGYEYKQGVQPIQGNENYLLQKCDNNKSCMDGNLVSPEKXPF 1693
 QY 880 -----TSLDVCPIYKCVLTKDNESLQDA 903
 Db 1694 GKVAHKYBEKCDYQGHKVPISIPPPPPVQOPQEPAPVTVYDVCSIV--KTLFKQTNPSDA 1752
 QY 904 CSLKYGANSRLKRCV---TPSGEPPT---SSRNKALICYPPRRRLYLTKIYDAWTKT 957
 Db 1753 CGLKY--GKTPSSKCCIPSDTKSGAGATGSGSDSISICPPRRRLYVYKQLEMTAL 1811
 QY 958 ESPQSGSEASSTGSGTTPPDSKEALLKAFVESAATFFPLMRYKKEBKVAOEGAGHG 1017
 Db 1812 --PQGBAAPSUSA-----DDLKNAFIQSAIITFFLMRYKKEBKPOG--DGSQQA 1860
 QY 1018 LPRVEE--GSPEYDPEDK--LKEGKIPDGFLROMFYTLGDRDILFSGSNDTTSVSKDTPS 1074
 Db 1861 LSQULTSYSDDEBPPPKLQNGKIPDPFLRMPTTLGDRDILVHGGN--TSDSGMTNG 1918
 QY 1075 SSNDNLKNIYVLASGSTEOERKKNKYKEI--KNFRCSTERSAPNLVSHQPTWENNKG 1132
 Db 1919 SNNN--NIVLEASGNKEBDMQIOEKIEQILPKNGGTPLVKXS--AOTPDKMMNBEAE 1972
 QY 1133 YIMHGWICALT---SKDKIAKVEKKPOKIEBENLMD---ANKK-----PKP 1175
 Db 1973 SIMKMTICALTYEKNPDTSAKDE---AKIBKDEYERKPGSTADKAGTASTPTGTYK 2029
 QY 1176 POYQYTNVLDENSSTSPRTTOQASDNTPTTLTHEVKAPTYRMEWGESFCRBRK 1235
 Db 2030 TOYDEKVLKEDTSG---AKTPSASDTP--LLSDVFLAPPYRYLBEWQONFCRKRKH 2083
 QY 1236 RLKQIKYDCVYENGDV-----RSGGGEACDSISTHDYSVPSFNCGCGKCHGSSY 1287
 Db 2084 KLAQIKHECVCYENGSGRRGIGITROYSGDEACENMLPKNDGTVPLEKPSCAKPCSSY 2143
 QY 1288 KMYTERKKEIFHQSNAVGOQKTDATRNNGTPEFKCFKTLTETPPDAKFLERLKNPCK 1347
 Db 2144 KMWIESKGEFEKQKAYEBOQ--DKCVNGSNKIDNGCEFLTLTSSSKAKDLKTL--GPKC 2200
 QY 1348 TNKEYGDDIDFEKDSKTPQHTTEYGPCKPKFTNQCQNGCVSGLANGCDGKSIDAKEI 1407

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Db 2201 PNNVEGKTFD--DDKTFKTKDODPCLKFSVNCCKDECD-NSKGTDCRNKNSIDATDI 2256
Qy 1408 AKMSSTDVVRYSDDNTNFEAGDLYKDACOHANIFKGIKIDVWKGYYGVGVDICEQTN 1467
Db 2257 ENGVDSTV-LEMRSASBSKSGFNQDGLNACRGAGIPBGIRKIDMKCRNVCGYVCKPEN 2315
Qy 1468 INERTDKEYVIGIPLFRWVENFLVDYKINDKISHCICKKESKCKINCCKNSKCLEK 1527
Db 2316 VNGBAKGHIIGIPLALVRWVEYFEDYKIKHISIRIKNGEISPCI---KN--CWEK 2369
Qy 1528 WIEKKIKWENIKKRFNDQYENKQOPDYKNSIIEELIPKIAVVDNDQNYIKLCVFNNSK 1587
Db 2370 WVDQKREWKSTIEFVKQYKNDNSDDNVSFLETLIPQITDANAKNKVTKLSKFGNSC 2429
Qy 1588 GCTTISNTQ--NNKENDADCMCLKLGVKAKNCPEK--PSEKQSDCKEPPPLPDE--- 1639
Db 2430 GCSASANQNKNGEYKXADICMLKKLKGCEKHHQISDTESDTPQQTLEDETLD 2489
Qy 1640 --EDQNEENTLEBPFCPT--TPPEKQGETCGNKEKKDKKESSEEPKESBGP 1694
Db 2490 DDIEBAKKNMM--PKICEVNLKTAQOEDEGC--C-----VPAENSEEPATDSGK 2537
Qy 1695 AAEAPAPASBETETNFEPPGTPGAPAPSTPA---PTEDTPPLRPQADEPDSCTL 1751
Db 2538 ETPQTPVLKPEEBAVPEPPPP-----PQEKAPAPLPQPPPTQLDNPHTAL 2591
Qy 1752 QT-TTFGVALAGSIAPFLFK 1772
Db 2592 VTSTLMSVGIGFATFYFLK 2613

```

RESULT 5 US-09-210-288-12

Sequence 12, Application US/09210288

Patent No. 6392026

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan

APPLICANT: Miller, Louis H.

APPLICANT: Peterson, David S.

APPLICANT: Su, Xin-zhaun

APPLICANT: Wellens, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe Martens Olson & Bear

STREET: 620 Newport Center Drive 16th floor

CITY: Newport Beach

STATE: California

COUNTRY: US

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/210,288

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Fuller, Michael

REGISTRATION NUMBER: 36,516

REFERENCE/DOCKET NUMBER: NIH121.1FWDV1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 2710 amino acids

TYPE: amino acid

STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYDROTHERMAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
US-09-210-288-12

Query Match 26.4%; Score 3197.5; DB 2; Length 2710;
Best Local Similarity 30.6%; Pred. No. 3.9e-203;
Matches 834; Conservative 244; Mismatches 569; Indels 1075; Gaps 74;

Qy 4 SGSGSGTQDEADAHVLDPEQGVHDEYHGRKXVYSELKSLASLISGTAFTVSMQT 63
Db 14 AAGGDDIEDSARHMFRIKIDVDYDKVEBAKERGKGLQRLS-----BAKEKESDP 67
Qy 64 ES-----KYTELEANSKRNPK-----KDGKNDVDRFSYKEQGYDNKKMKC 107
Db 68 QTEPDDCDLHKHTHTVTTN-VINPCADRDVAFPSDEYGGQCTHNRIKDSQGDNGK--- 123
Qy 108 SNGMTCAFFRRLHLCNKPFPNMSNDSSKAKHDLAECVAAYEGESITTHYPKTDSKY 167
Db 124 ----ACAPYRRLHYCDQNLQIEPIKITYNT-NHLLVDVCMAAFEEQGSITQDPKQATY 178
Qy 168 PGSDPWCMTLARSFADIGIIRGRDLYLGNKKKKQNGKETEREKLEQKLEIFKIHND 227
Db 179 GDSPSQICTMLASFADIGDIVRGRDLYLGNPQELK----QKQLENNLKITFGKIYEK 233
Qy 228 LKDEAKQRYNGDEDPNFYKLRDPMWTANREYWGAMTCSKELDNSYFRATCNDTQGP 287
Db 234 LINGAEH--RYG--NDPEFFLRDPMWTANREYWKAITGNAM--GNIFYPATCN---RG- 283
Qy 288 SQTNNKCRCDKGAANAKPKRAGDGVTVPTVFDYVPQYLRNFRFEAAEDFCRKKKKLE 347
Db 284 ERTKGYRCNDQ-----VPTFYDYVPQYLRNFRFEAAEDFCRKKKKIK 327
Qy 348 NLEKQCGKDKSDERYKCSRNGYDCBOTISRKGVHMGKCTGCFACSGSYEMINDQK 407
Db 328 DVKNCRGKDKEDRYKCSRNGYDCBOTISRKGVHMGKCTGCFACSGSYEMINDQK 387
Qy 408 QFDKQ-KYTKELI-----SDGGKKRAVAG--TTYREGEYSFYKELANDGYTDAF 456
Db 388 QFDKQKKYDBELIKYENGASGSGRQKRDAGTTTNYDYEKKFYDELKSEKRYDKF 447
Qy 459 LGLINNEKAKCDITD--GKINFEKYNVSGGVGSGGSGTNGENKGTFTYSEYC 516
Db 448 LEKLSNEICTKYVDEBEGTIDFKNVN-----SDSTSGASTVVEGQGFYRSKYC 498
Qy 517 QPCPDGCVQ--HGG--NOMEKTKYVKRMKSLYK--INGKVLILSLKVVXDMMI 569
Db 499 QPCPYCGKVNNGSSNEMEBKKN-GKCSGKLYEPKPKEGTTITILSGKHHD--- 554
Qy 570 LKKNMKEFCLTONSSDSVGSVVTGASGNSSEKELYDEMCKYKANEVQKVNQGEVEE 629
Db 555 IEBKLNFCDBEKNDITNSGSGSGTGGSGNSGQELIYEMKCYKGSDDVYKVGHDDEDE 614
Qy 630 DDELKAGGICILPNPKKNKEVSEAKSQQNHADIQTFPHDFYVYVAHMLKDSIHWRTK 689
Db 615 DYEVNNAAGGICILKQKKNKEBEGANTSKEPEIDQTFPHDFYVYVAHMLKDSIHWK-K 673
Qy 690 RLKSCISDGTMKC-RNGCNKKCDCEFEKVKYKQKTEKPKIKDHFPTQDGIPEGYFTLE 746
Db 674 KLQRCLONGNRIRKGNKKNNDCECFRWITQKDEGKIVQHKTONIYKRGSGSDNTAE 733
Qy 749 LI-----LKLQFLKED-----TEENTENSIDAEABELHGLIKLLENENNLAV 793
Db 734 LIIPDHVYVLYQNLQEEFLKQDSSEDASEBSNSLDABEABELHGLLEIIESEDNNGEAS 793
Qy 794 VNAG-TEQKTLMDKLNHLEINDATKCDPLPEEDK----- 828
Db 794 VGGVTEQKNIMDKLNVBEKDEADLCLEIHDEEBEKGDQNECIEGENFRYPGSGE 853
Qy 829 ----- 828

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Db 854 SGNRRYPLANKVAYOMHKAQTOLASRAGSALRGDISLAQFNKGRNGSTLKGQICKIN 913
Qy 829 -----SNGRSADPS-----PDFIF----- 843
Db 914 ENYNSDSKNGSGPCTGKHOGHGVNRIGTEWSNIEGKKOTSYKNVFLPPRRHMTSN 973
Qy 844 ----- 843
Db 974 LENDVGSVTKNDRASHSLLDGVOLAATAAEIIRKYKDQNNITQITPQQKQOEMNCR 1033
Qy 844 ----- 843
Db 1034 AVRYSPADLGDIIIRGDMWDEKSDTDETRLIIVFKNIKEKHGDKONPKYTGDESXCP 1093
Qy 844 ----- 843
Db 1094 AYKRLRADWMEANRHOVRANKCATKGIIICPMGVVDYIIPQRLMTEMAEMWYCKAOSOE 1153
Qy 844 ----- 843
Db 1154 YDKLKICADCMKSGDKCTOGVDGCGKCAACDKYKEIEKMEQMRKISDKYNLYLQ 1213
Qy 844 ----- 843
Db 1214 AKTTSTNGRTVYLGDDDPDYQOMVDFLPIHKASIAARVYKRAAGSPTEIAAAPIPTY 1273
Qy 844 ----- 843
Db 1274 STAGYIHOEIGYGGCOBOTOFCCKHGTSTSTTKENKEYTFKQPPPEVATACDINRS 1333
Qy 844 -----RPEEKED----- 850
Db 1334 QTEBPKKKEENVESACKIVEKILBGNKRTVGECPKESYIPDMDCKNINIDISHGACMP 1393
Qy 851 -----DEN-----EDDEDEVRD--- 863
Db 1394 PRROGLCLYIAHESQTENIKTDNLKDAFIKTAALFTLSMWYKSKNDSEAKILDRGL 1453
Qy 864 -----DEBTAKF-----TTEGS----- 875
Db 1454 IPSQFLRSWMTFGDYRDCINTDISKKONDVAKAKDKIGKFKSGSKSPSGLSRQEMW 1513
Qy 876 -----ATDT----- 879
Db 1514 KTNGBEIKWMLCALTKYVTDIDNKRKIKNDYSDKNQSONGNSLEEPAKPOFLMW 1573
Qy 880 ----- 879
Db 1574 IEMGBEFCAROKKENIIKDACNEINSTQCCNDAGHCNQAARAYQEVENKKKEFSQOT 1633
Qy 880 ----- 879
Db 1634 NNFVLKANVQODPEPKGYEYKDVQPIQNEEYLLQCKDNKSCMDGNVLSVSEKEXP 1693
Qy 880 -----TSLDYCPITGVKVLTKDNESLDA 903
Db 1694 GKVAHKTPEKDCYQGAHVPSIPPPPPVQPOPEAPVTVDCSTIV-TLTFDNTNNSDA 1752
Qy 904 CSLKYGNNRSRLGMRCV---TPSGEPT---SSDKGALCVPPRRRLYIKKIIVMATKT 957
Db 1753 CGLKY-GKTAPSSMKCIPSDTKSGAGATTGSGSGSICIPRRRLIYVGLQJOMFAL 1811
Qy 958 ESPQASSEASSTSGSTTPPSKELALFVESAALFTFPLMHRKYEEKKAAVQEGAGHG 1017
Db 1812 ---POEGEAPSHSRA-----DRLNAPFIOSAALFTFPLMDRYKEKKKQG-DGSQOA 1860
Qy 1018 LPRVBE--GSPYDEDEK-LKEGKIPDGFRLQMFYTLGIDYRDLFSSGNDTTSVSKDPS 1074
Db 1861 LSQLTSTYSDBEDPDKLQNGKIPPPFLMFTLGLDYRIDLVHGN--TSDSGNTNG 1918
Qy 1075 SSNDNLKNIIVLASGSTOEERKNKYEI--KNFRKSTERSAPNLVSHQPTWENNKG 1132
Db 1919 SNNN---NIVLEASGNKEDMKIQEKIQLIPKNGGTPLVPRSS---AQTPDKMNEHAE 1972

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Qy 1133 YIHWGVCALT---SDKTIAGVEKKPOKIENBENLMB-----ANKK-----PKP 1175
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Qy 1176 POYQYTNVLDENSGTSPRTTQTOASSDNPTTTLTHFVKRPTTYRMBEENGESFCREBK 1235
Db 2030 TOYDEBKVLJEDTSG-----AKTPSASSDTP-LTSDPLRPPRYRYLEWQONPCKKRKH 2083
Qy 1236 RLKQIKYDCVENDVG-----RCSGGEADSDISTHDYVPSNPNCGCGKHSSY 1287
Db 2084 KLAQIKHECVRENGSGSRGGITRQYSGDSEACENMLPKNDGTVPDLKESCKAPCSSY 2143
Qy 1288 RKMTERKKIEPHKOSNAYGOOKTDATRNNGTDPKFCCKTLETYPDAKFLERLKNPGPK 1347
Db 2144 RKMIESKKEPEKQEKAYEQCK-DKCVNGSNKHDNGCELTITTSKAKDFLKL--GPCK 2200
Qy 1348 TNKEYGGDDIDFEKDSKTPQHTYCGPCKFKTNQNGNCGVGLNGCDGDSKIDAKEI 1407
Db 2201 PNVGKTIIPD---DDKTFKHDKDCDPLKFSVCKKDECD-NSKGTDCRKNISIDATDI 2256
Qy 1408 AKRGSSTTDVVMRSDNDTTFEBGDLKDAQOHANIFKGIKQVYKGYGVGVDICEOTN 1467
Db 2257 ENGVDSTV-LEMRYASDSKSGFNGDGLBNACRGAGIEGIRKDKMCKRNVGVCYKCPEN 2315
Qy 1468 INERTDGEVYQIRALFKRWENFLDYNNKINDKISHCIIKKGSGSKCINGCEKNSKLEK 1527
Db 2316 VNGEAKGKHIIQIALYKRWVEYIFEDYNNIKKHISIRKNGEISPCl---KN--CYEK 2369
Qy 1528 WIEKKIAEWENIKKRFNDQYENKQDPYNNVKSILEBIPKIAVVDQDNVYKLCVFNENK 1587
Db 2370 WVDQKRKEMKEITERFDQYKNDNSDDNVRSFLETLIPQITDANAKNVIKLSKFGNSC 2429
Qy 1588 GCTILISTQ--ANKENDALDMLKGLGVYKANGCGK---BGEKQSDCKEPPPLPDE--- 1639
Db 2430 GCSASANEONNGYKQALDMLKLDKDKICECKRKHQTSDTCSPTQOTJLEDTLD 2489
Qy 1640 ---EDONBEENTLEPPKFCPT--TOPPEKGECTCGNKEBKDEKEESEEPKAEBSG 1694
Db 2490 DDITEBAKMM--PKICEVNLKTAQEDBG--C-----VPAENSEPAPATBSG 2537
Qy 1695 AAEPPAPTAESEETETNPPEBPCTGPAAPSTPAP---PTPDPPLPAPQADEPDSITL 1751
Db 2538 ETPQGTPLKPEEBAVBEPPP-----PQEKAPAPIPQPPPTPQLDNDHVLAL 2591
Qy 1752 QT-TIPFGVALLAGSIAPFLK 1772
Db 2592 VTSTLAWSVGIGFATFYFLK 2613

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RESULT 6
US-10-153-273-12
; Sequence 12, Application US/10153273
; Patent No. 6962987
;
GENERAL INFORMATION:
;
APPLICANT: Sim, Kim L.
;
Chinitis, Chetan
;
Miller, Louis H.
;
Peterson, David S.
;
Su, Xin-zhaun
;
Wellems, Thomas B.
;
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/153,273
 FILING DATE: 21-May-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/210,288
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Fuller, Michael
 REGISTRATION NUMBER: 36,516
 REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 12:
 LENGTH: 2710 amino acids
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEetical: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmodium falciparum
 SEQUENCE DESCRIPTION: SEQ ID NO: 12:
 US-10-153-273-12

Query Match 26.4%; Score 3197.5; DB 2; Length 2710;
 Best Local Similarity 30.6%; Pred. No. 3.9e-203;
 Matches 834; Conservative 244; Mismatches 569; Indels 1075; Gaps 74;

QY 4 SGGSGCTQDEDAKHYLDERCGKYHDEYGEAKNYVELKGLSLASIIIGETAFTYKSMQT 63
 DB 14 AAGGDIDEDSAKHMFDRIGKDVYDKVEAKEKRGKLGRLS-----EAKFKNESDP 67
 QY 64 ES-----KYTELIEANSKRNPCK-----KDGKGNVDVRFVSKEQAGYDNKKMK 107
 DB 68 QTPPEPCDLKHKHNVTNN-VINFCADBSVDVRFDEYGGCTHNRIRIDSQGDGK--- 123
 QY 108 SNGMTCAPFRLHLCKNKFPPNNSNDSKAKHDLAECMAKYGESIKTHYPKYSKY 167
 DB 124 ---ACAPYRLHVCDDQLEQIEPIKITVT-HNLLVDCMAAKFSGQSITQDYPKQATY 178
 QY 168 POSDPKCTMLARSPADIGDIIRGRDLYIGNKKKKQNGKETREKLDEOKLEIFKIHDN 227
 DB 179 GDSPOICTMLARSPADIGDIVGRDLYIGNPOEIK---QRQLENNLKTIFEKIYK 233
 QY 228 LKDKAOKRYNGDEDPNFKYKLRDWMWTANRETVMGAMTCSKELDNSSYFRATCNTDGOQ 287
 DB 234 LMGAR--RYG--NDPEFKLRDWMWTANRETVMAITCNAM--GNTYFHATC---RG- 283
 QY 288 SGTNHCRCRCDKGNAGKPKAGDGDVTTVPYFYVPOYLWRFEMAEADFCRKKKKKLE 347
 DB 284 ERTKGYCRCNDQ-----VPTYFYVPOYLWRFEMAEADFCRKKKKKIX 327
 QY 348 NLEKQCRGDKSDEYRCRNGYDCBQITSRKGYKRMKGCTDCFPAGCSYNNWIDNRK 407
 DB 348 DYKRCRCRGDKDKORYCSRNGYDCEKTRALGKLRYGKQICISCYACPYPYDWMINDKE 387
 QY 408 QFDKO-KKYTEI-----SDGGGRKRAVVG--TTKYGYEKSFEYKLNKNGYGVNAF 458
 DB 388 QFDKQKKYDEIKKYNKASGSGSRQKRAAGGTTTNTNDGYIKKKYDELANKSEYTVDKF 447
 QY 448 LKRLSNEEICTKYKDBEGTIDFKVNN-----SDSTSGASGTNVSQGTFRSKYC 498
 DB 517 QCPGCGVQ--HKGG--NOMEKTKYKRRNSKLYP---INGKVLILKSLKVVYKDMMI 569
 QY 499 QCPYCGVYKVVNGSSNMEERKN-GCKSGKLYEPKPKDKGTTITLIKSGKHDD--- 554

QY 570 LKKNMKFCLTQNSSDSVGSVTTGASGNSKEKELYDEWKCYKNEVQKVNQGEVER 629
 DB 555 IEEKLNKFCDEKNGDITNSGSGTGSGGNSGRQELYEEMKCYKGDVYVGHDEDEE 614
 QY 630 DDDBLKAGGLCTLPNKKKKEVSEAKSONNHADIOCTFPDFFYVVAHMLKOSIHRTK 689
 DB 615 DYENVKNAAGGCTLKKNKKNEBGGNTSEKRPDIQITFNPFYVVAHMLKOSIHK-K 673
 QY 690 RLKSCISDGKTMKC-RAGCNKKCDPEKMYKQKETEMKPIKDHKTOEGIPRGGYFTTLE 748
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 QY 829 ----- 828
 DB 854 SGNKRYPLANKVAYQMHNRKKTOLASRAGSALRGDISLAQFKNGRNGSTLKQICKIN 913
 QY 829 -----SGRSADS-----PDIFIP----- 843
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 QY 844 ---RPEEKED----- 850
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 QY 851 -----DEN-----EDDDEDEVRD--- 863
 DB 1394 PRQKLCIYTAHESQTEINIKTDNLKDAFIKTAAEFTFLSMOYYKSNDBEAKILDLGL 1453
 QY 864 -----DEETAKE-----TTGGS----- 875
 DB 1454 IPSQFLRSMVTFPGDYRDICLNTDISKQNDVAAKXDKIGKFPKSGSKSPSGLSRQEMW 1513
 QY 876 -----ATDT----- 879
 DB 1514 KTNGBEIKWMLCALTKXYTDTDNKRKIKNDYSYDVKNQSGNAPSLEFPAKQFLRM 1573
 QY 880 ----- 879
 DB 1574 IEMGBEPCAEKQKKNENIKDACNEINSTQOCNDAKHRCNQAQRAVQVYVENKKKEFFSGOT 1633

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QY 880 ----- 879
Db 1634 NNFVLKANVQDPPEYKGVKGVQVPIQGNBYLLQCKDNKKCSMDGNVLSVPKPKPF 1693
QY 880 -----TSLDVCPIVGVLTIKNESLQDA 903
Db 1694 GKTAHKYPEKDCYQKGVKVPSPPPPPVQPPAPATVTVVCSIV-KTLFEDTNTFSDA 1752
QY 904 CSLKAGNNRSLGWRGV---TPSGPPT---SSDNGKALCVPPRRRLRYIKKIVMAKRT 957
Db 1753 GGLK-KGTAPBSMWKCIPSDTYSKGATTKSGSDSGSICPPRRRLRYVGLQEMATL 1811
QY 958 ESPQASGEASSTSGSTTPDSKEALLKAFVESAIEFFLMHRYKEEKAVAQEGAGHG 1017
Db 1812 --PQEGAPSHSRA-----DLRRAFIQSAIEFFLMHRYKEEKAQVQ-DGSGQA 1860
QY 1018 LPRVEE--GSPRYEDK-LKEGKIPDGFRLQMFYTLGDYDILFSSGNDTTSVKDTPS 1074
Db 1861 LSQLTSTSDDEDPDKLQNGKIPDFLRIMFYTLGDYDILVHGQN--TSDSGNTNG 1918
QY 1075 SSNDLKATVLLAGSTQERKMKYKEI--KNFRKSTERSANLVSHQTMWENKX 1132
Db 1919 SNNN--NIVLEASGNKEDMOIKOIKIQLPKNGTEPLVPKS--AQTPDKMWNHAE 1972
QY 1133 YIMHGMVCAIT---SKDIAKGVKKPKQKTEINPENLME-----ANKK-----PKP 1175
Db 1973 SIMKMICALTYTEKNPPTSARGDE---NKIEKDEVEYEKFPFGSTADHGHTASTPTGYK 2029
QY 1176 POYQYTNVLDENSGTSPRTTQTOASSDNTPTTLTHFYKRPPTYFWEFWEBSFCRERK 1235
Db 2030 TQYDEYKVLBDTSG-----AKTPASSDTP-LISDFYLPRPYFYLEWQGNFCRKRKH 2083
QY 1236 RLKQIKVDCXKENGVG-----RCSGDGEACISISTHXYSTPSTNCPCCGKHCSSY 1287
Db 2084 KLAQIKHCKEYBENGSGSRGRTQYSGDEACNEMLPKNDGYDLKEBSCAPRCSY 2143
QY 1288 RKMIRKKIEBFKOSNAYGOOKTDATRNNGNTFDEFCETLETWDAKFLERLKNKGCK 1347
Db 2144 RKMIESKKEPEKQKAYEOK-DICVNGSNKHDNGFETLTTSSKADFLKTL--GCKC 2200
QY 1348 TNKEYGDDIDFEKDSKTFQHTYCGPCPKFTKNCQNGCGVSLNGNCDGDSIDAKEI 1407
Db 2201 PNNVEGKITFD---DDKTFKHDKCDPCIKFESVNCCKDECD-NSKGTDCRNKNSIDANDI 2256
QY 1408 AKMSSITDVVRVSDNDTTFEGDDLDACQHANIFKGIKRDVAKCGYVGVDCBOTN 1467
Db 2257 ENGVDSIV-LEMRVSADSKSGFNGDGLNACGAGIFGIRKDEKCRNVCGYVVCXEN 2315
QY 1468 INERTDGEKEYIQIRALFKRWENFLBEDYNKINDKISHGICKGEGSKCINGCKSKCLBK 1527
Db 2316 VNGEAKGHIIOIRALVGRWVYFEDYNKIKHKISHIKNGEISPCI---KN--CYBK 2369
QY 1528 WIEKKIAEMENIKKAFNDQYENKQPDVNVVSLBELPKIAVNDQDNVILQVFNENK 1587
Db 2370 WVDQKRMKHEITERFKQYKNDNSDDNVNSFLETLIPQITDANAKNVILSLFNGSC 2429
QY 1588 GCTLTISNTQ--NNKENDAIQKYLGVAKNCPGK---PSEKSGDCEKPPPLPDE--- 1639
Db 2430 GCSASANQNGKGEYKDAIDCMLKXKIGCECKKHQTSPTSCSDTPPOQTLDEDTLD 2489
QY 1640 ---EQGNBEENTLEPPKFCPT--TOPPEKGEFCGNKBEKDKKESSEEPAREESGP 1694
Db 2490 DDIETBEAKNNMM--PKICENVLKTAAQDEBGG--C-----VPAENSEPPALTDGSK 2537
QY 1695 AAEBPAPTAASEETETNPPEPGTGPAAAPSTPAP---PTPDTPLPLRQADPEPDSITL 1751
Db 2538 EHPEDQPVLPKPEEBAVBEPPPP-----PQEKADAPIPQPPPTPQQLDNPVLTAL 2591
QY 1752 QT-TIPFGYALALGSIAPFLK 1772
Db 2592 VTSTLAWSVGIGFATFYFLK 2613

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RESULT 7
US-10-087-013-2
; Sequence 2, Application US/10087013
; Patent No. 6855323
; GENERAL INFORMATION:
; APPLICANT: Arthur Scherf
; APPLICANT: Louis H. Miller
; APPLICANT: Benoit Gamain
; APPLICANT: Dior I. Baruch
; APPLICANT: Pierre Buffet
; APPLICANT: Christine Scheidig
; APPLICANT: Yurg Gysin
; APPLICANT: Bruno Pouvelle
; APPLICANT: No. 6855323utaka Fujii
; APPLICANT: Joseph Smith
; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; FILE REFERENCE: NIH176.001C1
; CURRENT APPLICATION NUMBER: US/10/087, 013
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/24195
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,023
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3542
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-087-013-2

Query Match      13.9%; Score 1681.5; DB 2; Length 3542;
Best Local Similarity 20.2%; Pred. No. 4,2e-102; Indels 1977; Gaps 136;
Matches 754; Conservative 327; Mismatches 680;

QY 13 EDAGVLDLDFGQK-HDEVGEAKNYYSELKGSLSLASILGETAFTVK----- 59
Db 33 KSANVLERYAKNIRHPSKY--AKENHDSLKGLDTKAEFRGSPSTPVNKHVYYPYPCNL 90
QY 60 --SMQTESKYTELIANSKRNPKCKKDGKNDVDPVSYEQAQYDNK---PKKCSNGMTC 113
Db 91 DHKEHTMLRYDDV---NLHPKC---HGRQNFDEDEBESBCNKLINRYRK-NDALAC 141
QY 114 APPRRLHCNKPFRMNSNDSSKAKHDLAVCAAKYEGSSIKTHYKYSKYGSPFP 173
Db 142 APPRRRHWCNDKLBALNDINTQNT-HDLGNVLTAKTEGESSIVNNHP-----HKGTIS-D 194
QY 174 MCTMLASFADIGDIINGRDLVGNKKKKKQNGKETEREKLBOKLKEIFKLIHDLKDKBA 233
Db 195 ACTALANSFADIGDIVKICIDHF-----KRVHDKVETGLREVKIKLHDGMD-BV 243
QY 234 QKRYNGDEDPNFFYLKREDMTANRETWGAMTCSKELDNSSYFRATCNDTGQSPQTHNK 293
Db 244 KNDVNPQSSGNYTLREAMNVMNKNKWEALITCDASY-KSGYFMQSEST--PLFSNPK 299
QY 294 CRCDKQKAGNAGKPKAGDGVTVIPTYFDYIPQTLRWEEBAEDPFCRKKKLEMLEKQC 353
Db 300 C-----GHKQK-----VPTMLDYPQYLRWDEWGEBCFRGNRLKLVKXQSC 343
QY 354 RGDKSDERYCSRNGVCEQTIISRKGKVRMGKCTDPCFACGSYENMIDNRKQDFDQK 413
Db 344 R-NDK--ERLYCSHNGHDCITTIKKGLIHLDNKCTDCTCKPFEVWLGNGQAEAFKQK 400
QY 414 -KYTKEISDGGGKRRKRAVGTTKYEGYEKSYEKLKNDGYGTVDAPLGLNNKCAKQIT 472
Db 401 EYKEKEIGSYLSDNKKFVNNIN--SEYKQFYELKETOYATNTDTFLALLNEGKCYCK-- 455
QY 473 DGGKINFKEVUNSGGCVGSGGTSAGSGTND-ENKGFYFYSYEQPDPDQGVQ----- 525
Db 456 -----GGLPGEKDIITFTNSADKGIIFYRSEYCVQVCPDGVKCDGIXY 497

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QY 526 -HKGQWNER-KTVKQKQWMSKLYKPIKNGKVVLLKSLKVVKDMILKQKKEFCLTQNS 583
 Db THKSDNBERVNNEDYKPPMG--VKPTN---ITVLYSGNEQD---ITQKLENNFC---NS 546
 QY 584 SDGSGSVYVTTGASGSEKKEKELVDEWKC-YKHEVQKVVNVQGEVDEDDDLKQAGGLCI 642
 Db 547 S-----TNYKDKNNQK-----WECYKDENINCKLEONTEINND----- 581
 QY 643 LPNPKKNEVSEAKSQNNHADIQKTFHDFYVWVAHMLKDSIHMRTKLSKSIDGKTMK 702
 Db 582 --NPK-----IISFHNFFELMVTYLLRDI KXMDK-LKTCINN-TTTH 620
 QY 703 CRNGKNCDCFEKAVKQKETEWPCKIDHFKTQSGIPREGY----- 743
 Db 621 CIDECNRNCLCFDRVVKQKEEEMWSIKKLFTKCKNIQOSYYSNINNLBEGYFFKVMKLD 680
 QY 744 -----FTTLE-----LILKQFLKE-----DTEBENTENS 767
 Db 681 KQBAKMKELMENIKRKQNEFSNLENNNDYLENAIELLDHLKETATTICKONNTWEACETS 740
 QY 768 LDA-----EBA----- 773
 Db 741 HNATTNPCVKPRGGTOPTKNIKEIQAQYKRSAYEABARRGLHKLKGAHBEIYKRGGRK 800
 QY 774 ----- 773
 Db 801 DKONLCRIMIGHSNRNLGFSNGPCDGKGTGDIQTRFVVGTEWVEDEHNRKDHEDYIM 860
 QY 774 -----BELKHQ-----KILKLENE--NUL 791
 Db 861 PPRRRHICTSNLEHLQTDHPLNGNI VDDL VYNSFLGCVLLSAKXEANKIIRMYEKNUL 920
 QY 792 AVVNAQTE--OKTL-----MDKLLNH----- 810
 Db 921 KQPKVETDPKHQOTTICRAIRYSPADIGDIRGRDLMERNKGMVKLOGHLETVFGIHKSL 980
 QY 811 -----ELN-----DATKCKDCPLPEEDKSRGRS-----A 834
 Db 981 KQKGNDKVNDAPKYLKLRNWMEMANRAKVMAMKCIKYL--KQKSGHQSQTOSYSGYS 1038
 QY 835 DQSP-DIFP-----RPEKEDE----- 852
 Db 1039 DHTPLDDYIPQKLRTWTEWAEWYCKVQKKEYDKLEKCKECKDKQKQGTCKESGTGCTK 1098
 QY 853 -----NEDD-----EDEVRDEETAKETTESATDTTSL----- 883
 Db 1099 CTBACNEVYDITGLMKEQWNIISDKYKEIHEQAQMSVNSGIBASTAKNHDRAVIBFL 1158
 QY 884 -----DVCPIVGKVL-----KD 896
 Db 1159 SELYOONGGKSNKSGTSDESAIVGTNTYENGAVYLHDTGNFDDCOQONEFCDEKSDGKD 1218
 QY 897 NESL-----QD--ACSLKYGANNRSLGRCVTS9GPTT----- 928
 Db 1219 NEKYAFRDKPQDHGACGCKSGSKPTRVQIKTKKAAEBKDTECKTVNDILKENDKKQVE 1278
 QY 929 -----SSDKNG-----AICVPRRRRLYIKKIIVDMATKTESPOASGBASS 969
 Db 1279 DCHPKKNSNGYPDWOCGNINLYEDPRVCHPPRRQKICHAFL-----ANDEIKK 1327
 QY 970 TSGSTTPPDSKEALLKAFVESAAIETFFLMHRYKEBKKAVAQBGAGHGLPRVEBGSPEYD 1029
 Db 1328 L-----QSOYVNLKAFIKSAAEFFFSMYKK-----SKDGSNELL----- 1363
 QY 1030 PEDKLEGGKIPDQFLRQMFYTTIGDYDILF----- 1059
 Db 1364 -KKELEGGKIPPAFLASMFYTTGDRDPLFGTDISKHGEGSKLKEQIDSLFRNGDQSP 1422
 QY 1060 ----- 1059
 Db 1423 NGKROEMWTEHSHEIWEMLCALVKIGAKKODFTENYGNVNVKSDKSTTLEBFAKPO 1482
 QY 1060 ----- 1059

Db 1483 FLRWLTWYDYCYTRQKYLKDVQEKCKSDQKCDTECNKKCBDYKTKMKKKKWTLPD 1542
 QY 1060 -----SGSNDT-----TSYSKDTPSASN----- 1077
 Db 1543 KYVYDERDKKRFDRQHGIGWVWTDYTGTMATDYLNRRKFTTACGQKPGSASVVGRIQLLEK 1602
 QY 1078 -----DNLKNTV 1084
 Db 1603 QAVYADKHGCTGFIENDDKYTNISSKDKCKGLVKEANTGAIKMNKGPNNYNNLKELT 1662
 QY 1085 -----LLASGSTE-----QREKKA 1098
 Db 1663 EDVLPSPRRRLICFHALDGYTTDPYKQENGLRKRLMEVAIATGNTNLGQYKKEKEKEKI 1722
 QY 1099 -----NKY-----KEINFRKCTERS 1115
 Db 1723 KTSDAHKIYSEVPPCSAMKYSFYDLRDIILGIDNLBEKQKTEBENLKKIFNKQTSYVGK 1782
 QY 1116 APNLVSHR-----QTMWENNGKXYIWHGMVCL----- 1142
 Db 1783 SDSGTGNPGSTARKFPWNENKECVMWNAIMCGYKRGGRDDGNSGNSARSDEDLKKGGSVPSD 1842
 QY 1143 ----- 1142
 Db 1843 DDYPMGNRDEGTAYOFLRWFPAWGEDPCRKKEKELEKLVGACNDYTCGDNEDRKRCCTD 1902
 QY 1143 -----TSKOKI-----AKGE----- 1153
 Db 1903 ACTQYKPFISWKQYQEKQIKKYEENDKIYSEHPVAKDAEABEYDKQKIKCENKSG 1962
 QY 1154 ----- 1153
 Db 1963 DCEYCKMKDVSTQRLTDGNSQNPASILDDEKBEVGEKGCQCPVPRGPRVRETPSPRVSL 2022
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 QY 1162 -----PENLMEANKKPK-----PQO-----XQYT 1181
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 QY 1198 -----TQASSP-----NTPPT----- 1208
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 QY 1209 -----LTHFYVRPTYFPMFEEWGESFCRERKJR 1236
 Db 2263 IYGLTYHLTDENEKEKIRDNQYNDMTKLTLSLEFYVRPOFLMFTMAEFCKNRKEQ 2322
 QY 1237 LKQIKVDCQVE--NGDVGRCSGDEBACDSISTHDYSTVPSPFCGCGHGSYRKMTERK 1294
 Db 2323 LKLEAGCKEYECNG--SNDGKQOE-----CAEACVYQNFILKWM 2360
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 Db 2361 KTEYERQREKPKQDKGKQYDYPSTERDIEKATCAHEYLMKLELGNKDCSQMOKPS 2420
 QY 1326 -----KTIETWPD----- 1333
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 QY 1334 -AAKFLER-----LKNGPCKTNKYEGD----- 1355
 Db 2481 KAAVYLSKEAENNDITLKEKFIPIESTYKESKNSWTNNNPCKPKYAPADKYIGRRNP 2540
 QY 1356 -----DIDFB--KDSKTFOHTE--YCGPCPKPFTINQNGNCGVSGJLNGNCDG-- 1398

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Qy 1399 DKSIDAEIAIAC-----RSSTTDVVMRV--SDN-----DTNTEGDDLKDAQOHAN-- 1442
Db 2590 ERLKDSNYLLKMWRTARNEGIDIIKNPNSGNCAMNDICDTMKYSPADLDIVRGDTML 2649
Qy 1443 -----IFKGI-----RKDVWKGYVCG 1459
Db 2650 RIGGVLPEVEIKLVFEYIYIGKMRNKNKGNKNKNDVOTPRSAMWDAKRIWK--AMTCK 2708
Qy 1460 VDICEQNTINERTDGE---YIQRALFK-----RVYENF-----LEDY 1495
Db 2709 APBDALKPRKGRMGDFERITLIDQCGHKKDPVDYIPQRFRTWTESEYCKALMBEL 2768
Qy 1496 NKIKDKISHCIKKGEGKICNCEGN--SKLEKIEKK--IAEMENI-----KGRFNQY 1547
Db 2769 EKFKKSCDHG---KTSRCKRDYBENKCEQCKTRCQEKYKLVKKSLSFDIQSNKYKELY 2825
Qy 1548 ENKQDPYVNVKSI---LEELIPKIAVNDQNVIKLCVF--ENSKGCTLISNTQNNKEN- 1601
Db 2826 E---QPIYTKISTYDHYQNFVQKLTFRKSECSVESFSFYHETSKCLNKNKENDGSSNI 2882
Qy 1602 -----DAIDCMLKGLGVKANCPCGKPSGEGKQSDCKEPPPL---PDEQON- 1643
Db 2883 RTVAFEETPKSYKCAKSCITLPSKN--PLDNC---PTDQKDGCKELQFTFPCSKNQDYDNL 2938
Qy 1644 -----PEENTLEPPK--FCP--PTQPPPEKG-----GCTC 1670
Db 2939 DNWNAVYLVNSSDNDKGLVLPFRRHLCITRBITAYNRKGGKEILKKLLTSAPSGQL 2998
Qy 1671 GNKEEKKOE-----KK--EESSE----- 1686
Db 2999 GQKTKSEBELCFEAMKTSYADYSIIKQTDMMOTSLSKIKKIFETSSEALENKRKTWEN 3058
Qy 1687 -----PAKESG-----PAEBSPPATASE 1706
Db 3059 NRQIWMHMLGQYKATSKVTLDEGWCQLPDEBEINQGLRWLIBWAKQACEKKHVPSL 3118
Qy 1707 ET-----ETNFP-----EPPG----- 1717
Db 3119 KTKCPRSNEDNFEASELIRQCGCONDIRKYSILNLIKNTMENLNKYYKQKQDSSGND 3178
Qy 1718 -----TGPAAPSTPAPT----- 1731
Db 3179 NKPSBENQSYIKSKQSCALELNDINEIYTGTKNENNEKFEYAKLUPGLYFVEDETH 3238
Qy 1732 -----PDPPELPAPQA-----DEFPDST-----ILQTTIPPGV 1759
Db 3239 KNHVLADGNIKKEBOGVTRPKALYFTRPHVDSFYQAPLFTTHVAQVDPKNDILKSSISVI 3298
Qy 1760 ALALGSIAPFLPKKTKKASVGNLFOILOIPKSDYDIPFLKSSNRYIPYVSDRYKGYTY 1819
Db 3299 VSAIGLILAHFMKKKFKGSV--DLARILNIPOGEYGMPTLESKNRYIPYRSGYKGYKTY 3357
Qy 1820 MEGGS--DEDKYAFMSDTTVDYSSSESEYEBELDINDIYVPGSPKYTLLEVLPEPGNNT 1877
Db 3358 MEGDTSYGEDYKMWDLSSDITSSSESEYEBELDINDIYVPGSPKYTLLEVLPEBKRDP 3417
Qy 1878 ASGKATPSPDTRNDQNDGIPSSKTIIDNEMNOLKKEFISNMLQON--QPNVDVPDYTSGNSST 1936
Db 3418 SD--DTFS-----NDTPRNRFTIDDEMELKHFQOYLPTNERN--NNYISADIPM 3465
Qy 1937 NTNITTTSRHVNNTNTTMSRDNMEENLLPSIHGULYSGEEYSYVNM--VNSMNDIP 1995
Db 3466 NTE-----PNTLYSDNPEEKPIIISIHDRDLTGKKEISYINIMNSTNTNDIP 3512
Qy 1996 INRDNNVSGIDLINDSL 2013
Db 3513 MNAARDSYRGIDLINDSL 3530

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; Sequence 10, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellems, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobb Martens Olsson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,459A
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelien, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; US-08-568-459A-10
Query Match 11.4%; Score 1385; DB 1; Length 700;
Best Local Similarity 40.8%; Pred. No. 2e-83;
Matches 328; Conservative 106; Mismatches 207; Indels 162; Gaps 34;
Qy 113 CAPRRLHLCKNKPNNNSNDSSAKADLAEVMAKYBESIKTHPKYDASKPRGSD 172
Db 10 CAPRRLHLCDY---NIESIDTSTHKLLEVCMAKYBENSINTHTYHQRNEDSAS 66
Qy 173 PMCTMLARSPADIDGIIIRGRDLYLG--NKKKKONGKETREKLBOKLKEIFKTH--DNLK 229
Db 67 QLCVTLARSPADIDGIDYRGKDLVYGYDKKESQ-----RKLKQKLDKIDFKLHKDVMK 120
Qy 230 DKEAQKRYNGD--EDPNFYKLREDMWTANRETVMGAMTCSKELDSSYFRATCNDTGQPS 288
Db 121 TNGAQERYIDAKGQDFQGLREDMTNSRETVWVALICHAKENYFIKTACN--VGKG-- 177
Qy 289 QTHNKKCDKDKGANAGKPRAGDGVITVPTFYFVYVPOYLRFMBEAMADFCRKKKKKLEN 348
Db 178 -TNGQCHC-----IGGD-----VPTYPYVPOYLRFMBEAMADFCRKKKKKLEN 220
Qy 349 LKQCRGKDSDEYRYSRNGYDCEQITISRQGYKRMGCGTDCFPAGCSYENMIDNORKO 408
Db 221 LQKQCRDVEON--LYSGNGYDCTKITIYKKGKLVIGHECTNGCSYCMETWTIDNQGKE 277
Qy 409 FDKQK-KYTKEISDGGG-----RKKRAVGSTTKYE--GYEKSFYKLNQDYGTVDAFLG 460

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Db      278 FLKQKRYETEISGGSGSKSPKTRARARSSSSDDNGESKFFYKJLKEVGVDVDFLK 337
Qy      461 LLNNEKACKDITDGGKINFEKVNSSGGVGGSGTSGASTNDENKGTFRYSYCOPCP 520
Db      338 ILNKEGICQKQPOVG--NEKADN-----VDFTNKKYVTFRTFTEICEPCP 380
Qy      521 DGVQHGKGNQMERKTKYKRWMSKLYPINKRVLLKSLKVVYKMMILKKMKFCLT 580
Db      381 MCGLE-KGGPPW--KVKGDKTCGSAKTKTYDPKNITDIPVLYPKSGQONILKTKNFC-- 435
Qy      561 QNSSDGVSQVYTTGASGNSKKELVDEMKCYKNEVQKYNVQGEVEDEDELKAGAGL 640
Db      436 -----EKAPGGGQIKK-----WCCTY-----DEHR----- 456
Qy      641 CILPMPKKNKEVSEAK-----SONNHADIQKTFHDFYYVAHMLKDSIMRTKRLKSGCI- 695
Db      457 ---PSSKNNNNCVBETMDKFTQKQKT--VKSYNVFMVMDMLHDSYEMKTE-LSKICIN 510
Qy      696 --SDGKTKCRNGCNKKCDCEKAVVQKETEWPRIKDHFKTQEGI-----PBGY 743
Db      511 NNTNGNCRNNNKKCTDCGCFQKVEKKQEWMAIKDHFGKQTDIVQKGLVFSPYG-- 568
Qy      744 FTTLLEILK---LQFLKEDTEENTENSLDAEBAELKHLKILKLENNMLAVNACTE 799
Db      569 --VLDLVLKGNLLQNIK-DVHGDT-----DDIKHKKL--LDEEDVAVVLGGKD 614
Qy      800 OKTLMADKLNLHNLNDATCK---DCPLPEEDKSRGRSADSPDIFIRP-----E 846
Db      615 NNTTI-DKLLQHEKQABEQCKQKQECCKQAQESGRSAETREDERTQGPADSAGEVEE 673
Qy      847 EKEDDENEDDEVRDDEETAK 869
Db      674 EDDDDYDEDDDDVQDVVDSV 696

RESULT 9
US-08-487-826B-10
Sequence 10, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chltnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SRP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121,001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 10:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; US-08-487-826B-10

Query Match 11.4%; Score 1385; DB 1; Length 700;
Best Local Similarity 40.8%; Pred. No. 2e-83;
Matches 328; Conservative 106; Mismatches 207; Indels 162; Gaps 34;

113 CAPPRRLHLCNKNFNNNSNSDKAKDILAEVMAKYGESIKTHYPKYDSKYPSDF 172
10 CAPYRLHLCDY---NLESIDTSTTKLLEVMAMKYGNSINTHYTHQRTNEDSAS 66
173 PMCTMLARSPADIGDIIRGDLVYG--NKKKQNGKETEBKLEQKLEIFKTIH-DNLK 229
67 QLCYVLARSFADIGDIYRGKDLVLYGDNKEKEQ-----RKLEQKLDIFPKLHKDVVK 120
230 DKEAQKRYNDG-EDPNVYKLREDWMTANRETWGMATCSKELDSSYFRATCNDTGGQPS 288
121 TNGAQERYIDAKGDDFPQLEBEDWMTSRETVMKALICHAPKEANYFIKTRCN-VKGG-- 177
289 QTHNRCRCDKDKGANAKPKAGDGVTVTPYDPVPOYLRFEMABDFCRKKKKKLEN 348
178 -TNGQCHC-----IGD-----VPTFYVPOYLRFEMABDFCRKKKKKLEN 220
349 LEKQCRGKDSDEYRYCSRNGYCEQITISRKQYRMKGCTDCFPACGSYENMIDNQKQ 408
221 LQKQCRDYEON---LYCSGNGYDCTKTIYKGLVIEHCTNCSVWRMETWIDNQKE 277
409 PDKQK-KYTKEISDGG-----RKKRAVGGTTYE--GYEKSFYKLNKDYGTVDAFLG 460
278 FLKQKRYETEISGGSGSKSPKTRARARSSSSDDNGESKFFYKJLKEVGVDVDFLK 337
461 LLNNEKACKDITDGGKINFEKVNSSGGVGGSGTSGASTNDENKGTFRYSYCOPCP 520
338 ILNKEGICQKQPOVG--NEKADN-----VDFTNKKYVTFRTFTEICEPCP 380
521 DGVQHGKGNQMERKTKYKRWMSKLYPINKRVLLKSLKVVYKMMILKKMKFCLT 580
381 MCGLE-KGGPPW--KVKGDKTCGSAKTKTYDPKNITDIPVLYPKSGQONILKTKNFC-- 435
561 QNSSDGVSQVYTTGASGNSKKELVDEMKCYKNEVQKYNVQGEVEDEDELKAGAGL 640
436 -----EKAPGGGQIKK-----WCCTY-----DEHR----- 456
641 CILPMPKKNKEVSEAK-----SONNHADIQKTFHDFYYVAHMLKDSIMRTKRLKSGCI- 695
457 ---PSSKNNNNCVBETMDKFTQKQKT--VKSYNVFMVMDMLHDSYEMKTE-LSKICIN 510
696 --SDGKTKCRNGCNKKCDCEKAVVQKETEWPRIKDHFKTQEGI-----PBGY 743
511 NNTNGNCRNNNKKCTDCGCFQKVEKKQEWMAIKDHFGKQTDIVQKGLVFSPYG-- 568
744 FTTLLEILK---LQFLKEDTEENTENSLDAEBAELKHLKILKLENNMLAVNACTE 799
569 --VLDLVLKGNLLQNIK-DVHGDT-----DDIKHKKL--LDEEDVAVVLGGKD 614
800 OKTLMADKLNLHNLNDATCK---DCPLPEEDKSRGRSADSPDIFIRP-----E 846
615 NNTTI-DKLLQHEKQABEQCKQKQECCKQAQESGRSAETREDERTQGPADSAGEVEE 673
847 EKEDDENEDDEVRDDEETAK 869
674 EDDDDYDEDDDDVQDVVDSV 696

RESULT 10

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US-09-210-288-10
; Sequence 10, Application US/09210288
; Patent No. 6392026
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Welleme, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbé Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; US-09-210-288-10

Query Match 11.4%; Score 1385; DB 2; Length 700;
Best Local Similarity 40.8%; Pred. No. 2e-83;
Matches 328; Conservative 106; Mismatches 207; Indels 162; Gaps 34;

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Db 278 FLKQKRYETEISGGSGSKSPKRTKRAARSSSSSDMDGYESKPYKLLKEVGYQDVDFLK 337
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Db 338 ILNKEGICQKOPQV--NEKADN-----VDFTNKKYTKTSRTICEPCP 380
Qy 521 DCGVQHKGNQWERKTYKTKRMSKLYPIGKRVLLLSKLVKDMMLKKNKPECLT 580
Db 381 WCGLE-KGGRPW--KVAGDKTCSAKTKTYDPKNITDIPVLVPPKSGQNLKTKKNC-- 435
Qy 581 QNSSDGSVGVVTTGASGNSSEKELYDEMKCYKNHEVQKVVQGVVEBDDDLKAGGL 640
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Qy 641 CILNPKKNEVSAAK-----SQNNHADIOTFHDFYYVAHMLKDSIHRTKRLKSGI- 695
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Qy 696 --SDGKTMKCRNGCNKKCDCEKVVKQETBWKPIKDHFKTOEGI-----PEGY 743
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Qy 847 EKEDDENEDDEDEVRDDEETAK 869
Db 674 EDDDDYDEDDDDVDVQDVSE 696

RESULT 11
US-10-153-273-10
; Sequence 10, Application US/10153273
; Patent No. 6962887
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Welleme, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbé Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,273
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FWDV1

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
us-10-153-273-10

Query Match      11.4%; Score 1385; DB 2; Length 700;
Beet Local Similarity 40.8%; Pred. No. 2e-83; Indels 162; Gaps 34;
Matches 328; Conservative 106; Mismatches 207;

QY 113 CAPFRLHLCKNKNPENNNSNDSSKAKHDLAEVCAAYEGESIKTHYPKYDSKYPGSDP 172
DB 10 CAPYRLHLCDY---NLSEIDTSTTHLLLEVCMAAYEGNSINTHTYQRTNEDSAS 66
QY 173 PMCTMLASFPADIGDIINGRDLYLG--NKKKKONGKETREKTLBOKLKEIFKTH-DNLK 229
DB 67 QLCYVLARSFADIGDIVRGKDLVGYDNKEKEQ-----RKLLECKLDIFKTHKDWK 120
QY 230 DKEQKRNQD-EDNPFKLRDMWTANRETYWGAMTCSKELDINSYFRATCNPTGQPS 288
DB 121 TNGAOSRYIDAKAGDFFQLRDMWTSRETYWKLICHAKREANYFIKTACN-VGKG-- 177
QY 289 QTHNRCRDKDKGANAGPKAGDGDVTIVPTVFPVLYLMFEEBMAEDFCRKKKKKLEN 348
DB 178 -TNGQCHC-----IGSD-----VPTVFPVQYLMFEEBMAEDFCRKKKKKLEN 220
QY 349 LEKQCRGKADDERHYGSRNGYDCQRTSRKQKVMKGCCTDCCFACSGSYEMIDNQKQ 408
DB 221 LQKQCRDEQN---LYCSGNGYDCRTKYKQKGLVIGHCTNCSYWCMEYETWIDNQKE 277
QY 409 FDKOK-KYTKETISDGG-----RKRAAGGTTKYR--GYEKSFEYELKNDGQGVDAFLG 460
DB 278 FLKQKRTETETISGGSGSGSPKRTKRAARSSSSSDNGYESKFTYKLEVGQYQDYDKFL 337
QY 461 LLNNEKACKDITDGGKINFEKVNSSGGVVGSGGTSAGSGTNDENKGTFFRSEYQPCP 520
DB 338 ILNKEGICQKQPVQ--NEKADN-----VDFNEXYVTFSTELCEPCP 380
QY 521 DCGVQHKGNOMERTKYKQKRMKLYPINGKMYLLKSLKVYKDMMLIKKMKKEFLT 580
DB 381 WCGLE-KGQPPV--KYKGDKTGSAKTYTPKNTIDIPVLYPDKSQONILKYKNFC-- 435
QY 581 QNSSGSGSVVTTGASGNSSEKELYDEMCKYKINNVQKVVQGEVEBDEDELKAGAGL 640
DB 436 -----EKDAPGGGQIKK-----WQCTY-----DEH----- 456
QY 641 CILPNPKIKKEVSEAK-----SQNNHADIOKTFHDFYYVAHMLKDSIHWTKRLKSCI- 695
DB 457 ---PSSKNNNNVEBETWDFKTOGKOT--VKSYNVFWDMVHMLHDSVEMKTE-LSKIN 510
QY 696 --SDGKTKCKRNGKCKDCFEKVKYKQKTEWPKIKDHFKTQEGI-----PBGY 743
DB 511 NNTNNTCRNNNKCKTDCGCFQKWKYKQKQEWMAIKDHFQKOTDIVQKGLVPSPYG-- 568
QY 744 FTTLLILK-----LQFLKEDTEENTENSLDAEABELHKLQILKENNNLAAYNAGTE 799
DB 569 --VLDLVLGNLNLQNIK-DVHGDT-----DIDIKHITKL--LDESDAVAVVLGKGD 614
QY 800 QKTLMDKILNHELNDATKCK---DCPLPEEDSKRGRSADPSPDIFIRP-----E 846
DB 615 NNTTI-DKLLQHEKEGAEQCKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 673
QY 847 EKEDDENEDDEDEVDDEETAK 869

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DB 674 EDDDDYDEDEDDDDVQDVVSE 696

RESULT 12
us-08-568-459A-8
Sequence 8, Application US/08568459A
Patent No. 5849306
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellem, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Knodde Martens Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459A
FILING DATE: 07-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
us-08-568-459A-8

Query Match      5.8%; Score 702; DB 1; Length 921;
Beet Local Similarity 26.2%; Pred. No. 8.1e-38; Indels 192; Gaps 28;
Matches 237; Conservative 131; Mismatches 346;

QY 1337 FLERLKNGPCCTNKYEGDDIDFEKDSKTFQHTYEGPCPKFKTNQNGNG-----VSG 1391
DB 12 FLNLKGGPCKKDNMDNEDNIDFQDBGTFEADNCKPCSGFTYDCKNCKNGDTRKQKNG 71
QY 1392 LINGCDDKSIDAKEIAMSSTTDVVMRVSDNDTTFEGDDLQDACAQHANIFGIRKDV 1451
DB 72 SNGKKNGNIDYITASDIENGNSINIDMVVSDKANGFNG---LDAGSANIIFGIRKEQ 128
QY 1452 MKCGYGVGVIDCEGTNINER--TDGKEYIOIRALFKGVENFLFDYNNKINDKISHCIK 1509
DB 129 WKCAKVGGLDVCGKANGSGIDKQKQIILIRALLKRWVEYFLSDYNNKINKAKISHCTK 188
QY 1510 EGSKINGCEKNSKCLEKWEIKKLAEMENIKKRENDQYENKQDPYVNVKSLIELIPKIA 1569
DB 189 NESTCTNDCPKCTCVEMINQKRTWMNLIKQHKITQNGENDN---NMKSLVTIILGLAQ 245

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Qy 1932 GNSSTNTTITTSRN-----YDNNTTTSRDMNEBNTLPSIHONLNTSGEYSYV 1985
Db 582 NNVPETHKIKITEGNNPEKVI FGSDSTLTSKSRBQFLRWLTWENANCKEOKEXK 641
Qy 1986 MNVNSMDIPINRDN-----NVSIGDILINDSISGKRPIDIYBELRK 2029
Db 642 VLLAKRCDCVDGDKCNGKCVACDKOCKQYHWSWIGIWDIYKKOKGRYTEVKKIPLYKE 701
Qy 2030 ENELFGTENYK---RTSTONVAKTINSPIPHOULEFKWLDRIHDMCEKKNK---ED 2082
Db 702 DKDVANSIDADLYLTQLONNKCVNGTIDENOCETCMKSTSTNSDMBSLDEKPEKYD 761
Qy 2083 ILNKLKEBMNKENINNSGKTYNSDNKPSHNHVLNTDVSIOIDMDNPKTKNEIITMDTNO 2142
Db 762 KNCVCPEBCNALSVSGSG---PPDQARFGGVLBGTCK---GLGEPKKKIEPPQYDPTND 815
Qy 2143 --KSTM 2146
Db 816 ILKSTI 821

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OY 1337 FLEFLKNGPCKTNKEYGGDIDFEKDKSTQHTYTCGPCEPKFNQONANG-----VSG 1391
Db 12 FLNFKLGKGPCKDNDNAEDNIDFDEBKETFEKANDCKPCSQFTVDCNKGSGDTKGKNG 71
OY 1392 LNGSCDDPKSIDAKEIANKMSSTTDVMMRVSDNDNTNFEGBDLKDACOHANI FKGIRKDV 1451
Db 72 SNGKKNGNDITLASDIENGNSISGIDMVSDKANGFNQ---LDAGSANI FFGIRKEQ 128
OY 1452 WKCGYVCGVDICEQTINER--TDGKEYIOIRALFKWENFELEDYNNKINDKISHCTKGG 1509
Db 129 WKCAKVCGLDYCGLXNGNGSIDKQKOIIRALFKWVEFFLEDYNNKINAKISHCTKXD 188
OY 1510 EGSICNGCENSGKCLEKYLEKLAEMENIKKRNQDYENMDQDYNYKSLIEBLIPKLA 1569
Db 189 NESCTCTDPCPKCTCVEBWINQKXTMEKNIKKHKTQONENDN--NKSJLVITLALQ 245
OY 1570 VVNOODNVYKLC-----VFENSGKCTLLSNQ--NNKENDAI DCMKKLGVAKKNPCKPS 1623
Db 246 PDSVNAKAIKCSGLTAFESFCGLANGDANSKGEGBDYDLVCLMLXNLEKIOGCK-KKH 304
OY 1624 GEK--QSDCKEPPPLPD--BEDQNPENTLEPPKFCPPYTQPEBKGGELTGKKEKXD 1678
Db 305 GETSVENQKSCSTPLDNTTLEBEPFIEBNOVEANICP-----KQTVED 348
OY 1679 EKKESEEPAAEBEGPAAEPAPFAEBSETTNPEPPTGTPAPAPSTPAPPTDTPP- 1737
Db 349 KKKKEEBETC-----TPASVPBEKPVH 371
OY 1738 -----LRPADPEPSTILQTTIPFGVALALSGIAFLPKKTKASVGM,FOLLOIPK 1790
Db 372 VAKRFTFPPEVPFKIMGRNRKTTCEI-----VAMLMDXNGRITTVGSCYR-----K 418
OY 1791 SDYDIPFLKSS---NRYIPVSDRYGKTYIYN--GSDDEDKIAFMSOTTDVT--- 1833
Db 419 ETVSEMTCDSEKIKMGCHGACIPPRQKCLCHYLEKIMTNTNELKIAFKCAAAETFLW 478
OY 1840 -----SSSEVEELD--INDIYVSGPKYKTLIEVLEPSGNNTTASOKTSPDTRDQ 1892
Db 479 QNYKKDKNGNAEDDEKLGKGIIPEDFGKQFY-----TFADYRDLCTL 521
OY 1893 NDGIPSKITTNENNOUKKEF-----ISNMLQONP-----DVPNDYTS 1931
Db 522 GTDLSKKDJSKGYGKVCNIDDPFYKISNIRKKSWMETNPGVIWGM,CALSYDSL 581
OY 1932 GNSSTNTNITTTSRH-----VDNNTNTMSRDMNEENLLPSIHGONLYSGEYSINV 1985
Db 582 NNVPETHEKLTLEGNNNEFKYIFGSDSSTLSKFSERPOFLRWLTWENBFCPEKDEKX 641
OY 1986 NMANSMNDIPINRN-----NVYSGIDLINDSLSGKRIPIYDEVLKRX 2029
Db 642 VLLAKCKDQVDGDKCKNGKCVACKDQCKQYHSHGWIWDYKKOKGHYTEVKKIPLYKE 701
OY 2030 ENELFGENTK---RTSTQNTAKTTNSDPPIHNOLELFPKWLDRHDMCEKWKNK---ED 2083
Db 702 DKDYVNSDADLYLKTQJQNMKCNVNGTIDENKCEYKCMHKSTSTSDWPESLDBKREKXD 761
OY 2083 ILNKLKEEWKENINNSGKTYNSDNKPSHNHYLNTDVISIQIDMDNPKTKNELLTMDTNDQ 2144
Db 762 KCNCVPECNALSVSGSG---FPDQAGGGVLEBCTCK---GLBEPKKKIBPPOYDPTND 815
OY 2143 --KSTM 2146
Db 816 ILKSTI 821

```

```

Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
Willems, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESS: Knobbhe Martens Olson & Bear
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-153-273-8

Query Match          5.8%; Score 702; DB 2; Length 921;
Best Local Similarity 26.2%; Pred. No. 8.1e-38;
Matches 237; Conservative 131; Mismatches 346; Indels 192; Gaps 28;

QY 1337 FLERLKNGPCKTKNKEYGDDIDPEKDSKTFQHTTEYCGPCPKFKTNGQNGCG----VSG 1391
DB 12 FLNLSKSGPCCKDDNADNIDFDGDEKTFEADNCKPCSQFTVDCNKNCGDTRKGKCGNG 71
QY 1392 LKNGCDGDKSIDAKEIAKRSSTTDVVMRVSDNDNTFEGBDLKDACQHANIFKGIKRDV 1451
DB 72 SNGKKNAGDYITASDIENGNSIGINDVVSDDKNGFNG--LDACGSANIFKGIKREQ 128
QY 1452 WKCGVVCVDICEQTININER--TDGEYIQIRALFKRWENFLBEDYNKINDKISHCIKKG 1509
DB 129 WKCAKVGGLDVGLKNGSGSIDKQKQIIRALLKRWVEYFLBEDYNKINKAKISHCTKDD 188
QY 1510 EGSKINCCEKNSKCLEKWEIKIAEWENIKKRFNDQYENKQDPDYNVKSLLEBLIPKIA 1569
DB 189 NESITCTNCPKCKTCVEEEMINQKTEWIKIKKHVKTQNGENDN--NMKSLVTDLGALQ 245
QY 1570 VVNODDNYIKLC---VFENSKGCTLLISNTQ--NNKENDALIDCMKKLGAKXNCPGKPS 1623
DB 246 PQSDVNAIKIPSGITAFESFGGLGADNSEKKGEDYDLVCMKLNLEKQIQECK-KKH 304
QY 1624 GEK--QSDCKEPPPLPD--BEDONPENTLEPPKFCPTTQPPREKGETCGNKEEKD 1678
DB 305 GETSVENGKSGCTPLDNTLTLEEBPIEENQVAPNICP-----KQTVED 348

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QY 1679 EKKESEEPAKESGPAABEPAPTAASEETETNFPBPPGTGPAPAPSTPAPPPDTPPP- 1737
DB 349 KKEESEEETC-----TPASVPKEKVPVH 371
QY 1738 -----LRQADEPPDPSTLQTTIPGVALAGSINFLPLKKTAKASVGNLPQILQIPK 1790
DB 372 VAWRTPTPEVEFKIMGRNNKTTCEI-----VAMLKDKNGRTTVGECYR-----K 418
QY 1791 SDDIPLTKS-----NNYIYVSDRYKGYIYME--GSDDEDKYAFMSDTTDTV----- 1839
DB 419 EYSEWTCDESKIMGQHACIPPRROKCLHYTEKIMTYINELKVAIFICAAAEFLWM 478
QY 1840 -----SSSEYEELD--INDIYVPGSPRYKTLIEVVLPESGNNTTASGKNTPSDTRNDIQ 1892
DB 479 QNYKKDKNGNAEPDDELTKGGIIPEDPKRMFY-----TFADYRQICL 521
QY 1893 NDGIPSKITPDNEMNQLKEP-----ISMLOQNP-----DVPNDYTS 1931
DB 522 GTDISSKQTSKGVGKVCNIDVIFYKINSIRKSMWETNGPVIWEGMLCALSYDPTSL 581
QY 1932 GNSSTNTNITTSRHN-----VDNNTNTMSRDNMEENILLPsiHNGNLYSGEYSYNV 1985
DB 582 NNVPETHKKLTTEGNNNFEKVIIPGSDSTLSKFSERPQFLRWLTWGENFPCKEQKKEYK 641
QY 1986 NMVNSMDDIPINRDN-----NYSGIDLINDSLSGKPIIDYDEVLRK 2029
DB 642 VLAKCKDCCVDGDKNGKCVACKOCQOYHSIGIWINYKKQKRYTEVKKIPLYKE 701
QY 2030 ENELFGENTK--RISTONVAKTTNSDPIHNOLELFKXMLDRHRDNCERKKNK----ED 2082
DB 702 DKDYKNSDDARDYLKTOQLNMKKCVNGTTDENCEYKCMHKTSSSTNSDPESIDEXPEKVKD 761
QY 2083 ILAKLKEENKKNENINNSGKTYNSNKSNNHVNLTVDVSIQIDMDNPTTKNIEITMDNOD 2142
DB 762 KCNCVPRPCALSVSGS---FPDGAFGGVLEGTC---GLGEPKKKLEPPQYDPTND 815
QY 2143 --KSTM 2146
DB 816 ILKSTI 821

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Search completed: December 29, 2005, 23:17:17
 Job time : 100.84 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 23:15:07 ; Search time 242.987 Seconds
(without alignments)
3831.174 Million cell updates/sec

Title: US-09-508-967-1
Perfect score: 12100
Sequence: 1 MATSGSGSGGTDEDAKHVLD.....VNNKKEIFEEERYPSIDIWNI 2228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3197.5	26.4	2710	US-10-153-273-12	Sequence 12, Appl
2	1681.5	13.9	3542	US-10-087-013-2	Sequence 2, Appl
3	1385	11.4	700	US-10-153-273-10	Sequence 10, Appl
4	702	5.8	921	US-10-153-273-8	Sequence 8, Appl
5	445	3.7	311	US-10-087-013-10	Sequence 10, Appl
6	439.5	3.6	407	US-10-087-013-8	Sequence 8, Appl
7	422	3.5	294	US-10-087-013-7	Sequence 7, Appl
8	421.5	3.5	1421	US-09-924-154-13	Sequence 13, Appl
9	418	3.5	1435	US-10-153-273-4	Sequence 4, Appl
10	414	3.4	1985	US-10-732-923-3351	Sequence 3351, Ap
11	396	3.3	1086	US-09-924-154-15	Sequence 15, Appl
12	395.5	3.3	6761	US-10-732-923-15035	Sequence 15035, A
13	386	3.2	308	US-10-087-013-11	Sequence 11, Appl
14	379.5	3.1	362	US-10-153-273-18	Sequence 18, Appl
15	376	3.1	1501	US-09-924-154-17	Sequence 17, Appl
16	376	3.1	1568	US-10-712-533A-12	Sequence 12, Appl
17	375	3.1	351	US-10-087-013-9	Sequence 9, Appl
18	371.5	3.1	1143	US-09-924-154-14	Sequence 14, Appl
19	371.5	3.1	1210	US-10-677-980-2	Sequence 2, Appl
20	360.5	3.0	411	US-10-153-273-19	Sequence 19, Appl
21	347	2.9	2399	US-10-732-923-15036	Sequence 15036, A
22	346.5	2.9	2719	US-10-732-923-8668	Sequence 8668, Ap
23	345.5	2.9	749	US-10-153-273-6	Sequence 6, Appl
24	324.5	2.7	616	US-10-293-913A-4	Sequence 4, Appl
25	323.5	2.7	616	US-10-293-913A-2	Sequence 2, Appl
26	322.5	2.7	2548	US-10-732-923-15009	Sequence 15009, A
27	320	2.6	2910	US-10-732-923-3342	Sequence 3342, Ap

28	315	2.6	1115	4	US-10-153-273-2	Sequence 2, Appl
29	295.5	2.4	5176	4	US-10-437-963-150986	Sequence 150986, A
30	288	2.4	2165	5	US-10-732-923-13547	Sequence 13547, A
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33	281	2.3	2133	5	US-10-732-923-15030	Sequence 15030, Ap
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35	277.5	2.3	2454	5	US-10-732-923-8884	Sequence 8884, Ap
36	276.5	2.3	2539	5	US-10-831-070-6	Sequence 6, Appl
37	274	2.3	3111	6	US-11-097-143-7773	Sequence 7773, Ap
38	273	2.3	4498	4	US-10-712-124-68	Sequence 68, Appl
39	273	2.3	4498	6	US-11-097-143-2577	Sequence 2577, Ap
40	273	2.3	10203	4	US-10-661-809-23	Sequence 23, Appl
41	272.5	2.3	2907	4	US-10-754-342-1	Sequence 1, Appl
42	272	2.2	10203	4	US-10-724-972A-4098	Sequence 4098, Ap
43	271	2.2	6641	4	US-10-282-122A-70580	Sequence 70580, A
44	269.5	2.2	2492	5	US-10-732-923-8882	Sequence 8882, Ap
45	269.5	2.2	2492	5	US-10-934-998-76	Sequence 76, Appl

ALIGNMENTS

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RESULT 1
US-10-153-273-12
; Sequence 12, Application US/10153273
; Publication No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
Chitnib, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
Wellens, Thomas E.
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1EMDVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum

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SEQUENCE DESCRIPTION:	SEQ ID NO:	12:
US-10-153-273-12		

Query Match	26.4%	Score 3197.5	DB 4	Length 2710
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Best Local Similarity 30.6%; Pred. No. 1,4e-156; Indels 1075; Gaps 74
Matches 834; Conservative 244; Mismatches 569;

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OY 64 ES-----KYTELIEANSKRNPK-----XDKGNADVRSFKVQAGYDNKMKC 107
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 QTPEDPCDLDHKHYHNVTTN-VINPCADSDVRFSDVEGGQCTHNRINKDSQGQDNKG--- 123
OY 108 SNGMTCAPRRRLHLCNKFENNNNSDSSAKKIDLAEVMAAKYBGESEIKTHPKYDSTX 167
Db 124 ---ACAPYRRLHVCDDNLEQIEPIKITPT-HNLVDVCMAAKFEGOSITODYPKYQATY 178
OY 168 PGSDPFCMCLMARSPADIGDII RGRDLVYGNKKKKQNGKETREBEKLEQKLEIFPKYIHON 227
Db 179 GDSPEQICTMLARSPDIDIGRGRDLYGNPOEIK---QRQJLENNLKITFGKITYK 233
OY 228 LKDKAEAKRYNGDEDEPNFYKLREDWMTANRETVWGMATCSKEIDNSSYFATCNDPTQGP 287
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OY 408 QFDKO-KYVTKEI-----SDGGGRKKRAVGG--TTYBGEYKSFYKLNQDGYTVDAF 458
Db 388 QFDQKKKKYDEIKKYEENGASGGSRRKDAAGTTTNNYDGEKKFYDELNKSRYRTVDF 447
OY 459 LGLNNKRAKCRITD--GGKINPKFVNSGGGVVGGSGTSGASGNDNKGKGFYSEXC 516
Db 448 LEKLSNEELCTYKQBEGGTIDFKNNV-----SDSTSGASGTVNESQGTFFYSKTC 498
OY 517 QCPDPCGVQ--HKGG--NOMERTKYKQKRWSLYKRP---INGAKVLLLSLKVNDMMI 569
Db 499 QCPYCGVYKANNSSNMEBEKN--GCKSKGLYEPKDXBGTITTLILKSGKHND--- 554
OY 570 LKKNMKEFCLTONSDGSVGSVYTTGASGNSSEKELYDBMKCYKENEYQKVNVGEBE 629
Db 555 IREKLNKFCDEKNGDTINSGGSGTSGGSGNSGRQLYEBMKCYKEDDYKV/GHDEDES 614
OY 630 DDELKAGAGLCILPRPKKKEKESLAKSQNNHADIOKTHDPFYVVAHMLKDSIMHRK 689
Db 615 DVENVYNAAGLCILKNQKKKKEEGGNTSEBDEPEIOKTPNPFYVVAHMLKDSIMHK-K 673
OY 690 RLKSCISDQTKMKC-RNGCNKKCDCEKXVVKQETEMKDIKHFKTOEGIPBEGYFTTLE 748
Db 674 KLQRCLOGNRRIKCGNKNKNNDCECFKRIIYQKKDMGKIYQHFKYQNIKGRGSDNTAE 753
OY 749 LI-----LKLQFLKED-----TEENTENSLDAEAEELIKHLQKLIKLENNNLAV 793
Db 734 LIPFDHYVLQYVLOREPLKGSSEDSAESEKSENSLDAEAELELHLREIIESEDNNOQAS 793
OY 794 VNAG-TEOCTIMDKLINHLELNDATKQCDPLREBK----- 828
Db 794 VGGVTEQKNIIMDKLINYKEDADLCLEIHEDESEKKEKQDNECTEBGENFRYPNCSGE 853
OY 829 ----- 828
Db 854 SGNKRYPLVLANKAYAOHMHKAKTQLASRAGRSLYLRDII SLAQKNGRNGSLTKGQICXIN 913
OY 829 -----SRGRSADPS-----PDIFIP----- 843
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Db	914	ENYSDNRKNSGGCGTCKDGDHGVRRIRIGTSMENISGKKQTSYKXVFLPBRREHCTSN	973	843
Qy	844	----	843	
Db	974	LENLDVGSVTKNDKASHSLLDVQLAAKTPAAEIIKRYKQNNIQLTDP10QKXQDAMCR	1033	
Qy	844	----	843	
Db	1034	AVRYSFADLDGIINGRDMWDEKDSSTMETRLITVFPKNIEKKHGDIGIDNPNPYTQDESKP	1093	
Qy	844	----	843	
Db	1094	AYKKLRADWMEANRHHQVRAKKAATKGIICGMVVDYIIPQRLMTEMAEWYKAQSOE	1153	
Qy	844	----	843	
Db	1154	YDKLKICADCMKSGDKCTQGDVDCGKCAACDKYKBEIEKNNEOWRKISDKYNLLYLQ	1213	
Qy	844	----	843	
Db	1214	AKTSTNPGRTVLDDDDPDYQOMVFLTPHKASIAARVLVKRAAGSPTEIAAAPTTPY	1273	
Qy	844	----	843	
Db	1274	STAGYIHQETIGYGCQEQOTQFCCKGKGAISTTTKKNKXETFFKQPPREYATACDINRS	1333	
Qy	844	--RPEEKD--	850	
Db	1334	QTEPKKKKEENVSACKIVELKLGKNGRTTVGECNPKESYPDWCKNNIDISHDGA	1393	
Qy	851	----	863	
Db	1394	PRROKCLYYTAHESQTEBENIKTDNLKDAFIKTAAEFTLSWQYKKSNDSEAKILDRGL	1453	
Qy	864	----	875	
Db	1454	IPSOFLRSMWTTFGDYRIDCIANTDISKKQNVAAAKXKJGFFSKDGSKSPGLSRQEMW	1513	
Qy	876	-----ATDT-----	879	
Db	1514	KTNGBEIKWGMICALTKYVTDTDNKRKIKANDSYDKVNQSQNGNPSLEBPAKQFLRMW	1573	
Qy	880	----	879	
Db	1574	IEWGEFCAEROKKENIIKDACEINSTQOCNDAKHRCNOACRAYOEVENKKKFE	1633	
Qy	880	----	879	
Db	1634	NNFVLKANVQPDPEYKQYKQVPIQGNBYLLQCKDDNNKSCSGMDGNVLSVPKXEPF	1693	
Qy	880	-----TSLDVCPIVGKVLTKDNESLQDA	903	
Db	1694	GKVAHKYPEKDCDYQKHPVSLPPRPVPQOPQEPATVTVVQSAIV--KTLFKDNTNNSDA	1752	
Qy	904	CSLKXGGNNSLGRVCV---TPSGEPT---SSDKNGALCYPPRRRLYIKYIDMA	957	
Db	1753	CGLKT--GKTAASSWKCIPSDTKSGAGATGKSGDSGSI	1811	
Qy	958	ESPOASGSEASTSGSTTPPDPSKEALIKAFYESAAIEFTFLMHYKKEKKRVAOEGAGHG	1017	
Db	1812	--PQEGGAPHSRA-----DGLRAFIQSAIIEFTFLMDRYKEKKRQG--DG9GQA	1866	
Qy	1018	LPRVVE--GSPBYDPEDK-LKRGKIPDGLRQMFYLLGDYRDLFSGSNDTTSVSKDTPS	1074	
Db	1861	LSQLTSTYSDBEDDPDLTLQNGKIPRPFLLMFYTLGDYDLVHGN--TSDSGNTNG	1918	
Qy	1075	SSNDNLKNIIVLLAGSSTQEBERKANKYKEI--KQFRKSTERSAPNLVSHQOTWENNGK	1133	
Db	1919	NNNN--NIVLEASGNKEDMOKIORKIEQIILPKNGSTPLVPKS--AQTDPKWNHEAE	1972	
Qy	1133	YTHHNCVALT-----SKDKIAKGYKKRQKILENPNLME-----PKP	1175	
Db	1973	SIWKMGICALYTKKNPJTSAAGDE--NKIEKQDEVLEKFFGSGTADHAGTASTPTGTYY	2028	

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Qy 1176 Poyoytnvklbnsngtsprtotoasndntptllthfvykrrptvfwfemgesfcrekx 1235
Db 2030 TQYDYKVKLEDTSG-----AKTPASDTP-LISDFLRRPFRYBLEBQNKCKKRAH 2083
Qy 1236 RLKQIKYDCKYENDVG-----RCSGDGEACDSISTHDYSTVPSFPCGCGKRCSSY 1287
Db 2084 KLAQIKHECKVEBNGGSRGGITRQYSGDEBACENMLPKNDGTVLPDLEKSCAKPCSSY 2143
Qy 1288 RKMIFERKKIEFHKGSNAYGQKTDATRNNGTFFDEKFKTLETWPAKFLERLKNCGCK 1347
Db 2144 RKMIESKKEPEKEKAYEOKK-DCCVNGSNKNDHGFCELTLTSSKADPLKTL--GPCK 2200
Qy 1348 TNKXEGDDIDPEBKSKTFQHTBYGCPKPKFTQNCQNGCVSGLNGCDGSDKSIDAKEI 1407
Db 2201 PNNVKGKTFP--DDKTFKTKDCDPLKFSVNCCKDECD-NSKGTDCRKNKSIDADYI 2256
Qy 1408 AKMSSTTDVVMRVSDNTNTEFGDDLDKACQHANIFKGIKRDVWKCVCYGVGVDICEQTN 1467
Db 2257 ENGVDSTV-LEMVRSADSKSGFNGDGLNACRGAGIFEGIRKDEWKCANNVGVYVCKPEN 2315
Qy 1468 INERTDGEYIYQIRALFRWYENFLDYNKINDKISHCICKKGEKSCINCCKKSKLEK 1527
Db 2316 VNGEAKGKHIIQIRALVGRWYEFEDYNKIKKHISHRIKNGEISPCTI---KN--CYEK 2369
Qy 1528 WIEKKIAMENIKKRFNDYENKQPDYNVKSLIEELPKIAYVNDQDNVTKLCVFEKSK 1587
Db 2370 WVDKQKREWKETEFKQYKNDNSDDNVRSFLETLIPQITDAKAKKVKIKLSFNGSC 2429
Qy 1588 GCTTISNTQ--NNKENDADICMLKLGAKKCPK---PGEKQSDCKEPPPLPDE--- 1639
Db 2430 GCSASANQNGKNGEYKQKIDCMKLGKIKGICEKGGHQTSDTBESDTPQGTLEDETL 2489
Qy 1640 --EDQNEENTLEBPFCPT--TPPEKGGETCGKKEKQKKESEBPAKESGP 1694
Db 2490 DDITEBAKMM--PKICEVNLKTAQOEDEGG--C-----VPANSEBPAATOSGK 2537
Qy 1695 AAEBPAPAESEETNTEPPEPGCPAPAPSTPAV---PTDTPPLRPAQADEPDSITL 1751
Db 2538 ETPEQTPVLPKEBEAVERPPPP-----PQEKAPAPLPQPPPTQLLDNPHVLTAL 2591
Qy 1752 QT-TIPGVALALGSIAPFLPK 1772
Db 2592 VTSTLAWSVGIGFATFTFYFLK 2613

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; SEQ ID NO 2
; LENGTH: 3542
; TYPE: PR
; ORGANISM: Plasmodium falciparum
US-10-087-013-2
Query Match 13.9%; Score 1681.5; DB 4; Length 3542;
Best Local Similarity 20.2%; Pred. No. 7.66-78;
Matches 754; Conservative 327; Mismatches 680; Indels 1977; Gaps 136;
13 EDAGVHIDFEGQKY-HDEVHGEANVYSELKSLASLIIGETAFYTK----- 59
Db 33 KSANVLEKAKNIRHPSKY--AKEHVDSLKGDITLTKAFRGPSTPVKNHNYYPYPCNL 90
Qy 60 --SMQESKYTELLEANSKENPCCKDGKNDVDHFSVYEOAGYDNK---KMKCSNGMTC 113
Db 91 DHKEHTLRYDDV---NLNHPK---HGEQNFDEBSECCNKIRYK--NDALAC 141
Qy 114 APFRRLHLCNKNFPMNNSNDSSKADHDLAEVCAAYEGESIXTHYPKYDSKYPGSDFP 173
Db 142 APPRRRMCDKNLEALNDINTQNI-HDLGNVLTAKYEGESIVNNHP-----HKGTS-D 194
Qy 174 MCTMLASPADIGDIINGRDLYLGNKKKKQKQKETERBKLEQKLEIPKTIHNLKQEA 233
Db 195 ACTALASPADIGDIVGIDMF-----KENVHVDKVEYGLREYFKKIHDMED-EV 243
Qy 234 QKRYNGEDRPFYLLREDWVTANRETYGAMTCKELDNSYFPAATCNDTCQGPSQTHNK 293
Db 244 KNDYNPDSGSGNYTLRANMNVNKNWEALITDASY-KSGYFMQSSNT---PLFSNPK 299
Qy 294 CRCDKDGANAAGKPKADGVTIVPTFYFDVVPQYLRWFEEWABDFCKKKKLEMLEKQC 353
Db 300 C-----GHQKQ-----VPTMLDYPOLYLRWFDEGEFCKRKNIKLKVADSC 343
Qy 354 RGKQDSERYCSNGYDCEQTSIRKGVKRMGKCTCPFAAGSYENWIDNOKOPDKOK 413
Db 344 R-NDK--ERLYCSHNGHDCITTIWKGIILHNDKCTCSTCKKFEVWLGQOEAFFKQK 400
Qy 414 -KYTKELISDGGGRKRAVGGTTKYEKESFYELKNDGVTQVAFGLNNEKACQDIT 472
Db 401 EKEKEIOSYLSNDNKKVNNIN--SEYKQYELKCTQYATNTFNLNLEGKYCK-- 455
Qy 473 DGGKINFKEVNSGGGVGSGGTSAGSTND--ENKSTFYRSEYQCPDQGVQ----- 525
Db 456 -----GGIPEKQDITFTNSADKQIFRSEYCYQCPDQGVACDGIKY 497
Qy 526 -HKGNQMER-KTKYKQKRWSKLYKPIINGKNVLLKSLKVVKDMMLKKNKEFCLTQNS 583
Db 498 THKSDNDRERVNNEYDKRPMG--VKPTN---ITVLSGNEQGD---ITQKLENFC--NS 546
Qy 584 SDGSVGSVTTGASGSGSEKKELYDEWKC-YKNEVQKNAVQSEVEDDELKAGAGICI 642
Db 547 S-----TNYKKNQK-----WECYKQENIRCKLEQNTLEINN----- 581
Qy 643 LPNFKKKEVSEAKSQNNHADIQKTFHDFFYVVAHMLKDSIHRTKRLKSCISDGKTMK 702
Db 582 --NPK-----IISFNPFELWVTTILRDTIKNDK-LKTCINN-TTTH 620
Qy 703 CRNCKNCKDCFEKMKVQKQETEMKPIKDHFTQDGIPEGYY----- 743
Db 621 CIDECNNCLCFDRWVQKEBENSICKLFTKKKNIQOQSYNSINNLPEGYFFKVMGLD 680
Qy 744 -----FTTLE-----LILQQLPKE-----DTEENTENS 767
Db 681 KDEAKWELMENIKKKNKEFSNLENNDYLENALTELLDLHDKETATYCKDNNTNEACETS 740
Qy 768 LDA-----EEA----- 773
Db 741 HNAITTNCAVPRGQGTQTKNIKEIAQYFKGSAYEAAKRGHLKKGAKHGGIYKRGGRK 800
Qy 774 ----- 773
Db 801 DFKDNLKIMIKHSNRMILGFSNGPCDQKGTGDIQTRFVVVGTWEVDPEHMKDHEVIM 860

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QY 774 -----BELKLO-----KILKLENE-NNT 791
Db 861 PRRRHICTSNLEHLOTDHPLANGNIYDDLNNNSFLGDLVLSAKYEANKIIRMYKEKNL 920
QY 792 AVNAGTE---OKTL-----MDCLLNH----- 810
Db 921 KGPKEVTDPKHOTYICRAIRYSFADIGDIIRGRDLMEBNGDMVKLOGLLETVFQNIHKL 980
QY 811 -----ELN-----DATCKDCPLPEBDSKGR8-----A 834
Db 961 KKGKNDKYNDAFKLKLRENNWENAKWEMAKCDIKYL--KDSGHSOSTOSSYCGYS 1038
QY 835 DPSP-DIFP-----RPEKEKDE----- 852
Db 1039 DHTPLDDYIPOKLRMTTEMAEWYCKVQKEVDKLKECKECKDKONGQCTKESGTGCTK 1098
QY 853 -----NEDD-----EDVRDETAETTESATDTTSL----- 883
Db 1099 CTEACNEYNDIIGLWKEQWNIISDYKELHBOQMSVNSGIEASTAKNHIDRNVIEFL 1158
QY 884 -----DVCPYGVLT-----KD 896
Db 1159 SELVQNGCKSKSGTSDSASAVIGTNTTYENVGAYLHDTGNPDCQSONEFCDEKSDGD 1218
QY 897 NESL-----OD--ACSLKYGNNSRLGWRCTPSPGPTT----- 928
Db 1219 NBKTAFRDPODHGACCGCKSGSKPTRVQIKTKKAEKDETECKTVNDILKENDOKQVE 1278
QY 929 -----SSDKG-----AICVPRRRRLYIKKIYDVAKTESQASSESS 969
Db 1279 DCHPKNSNGPYDMOCGNINIVEDPRVCPPRRQLCVHFL-----ANDNEIKK 1327
QY 970 TSGSTPDSKALIKAFVESAAIETFLMRYKEKKAVAOEGAGHGLPRVEGSPREYD 1029
Db 1328 L-----QSOVNLKBAFIKSAHAETFPSSWYTK-----SKDSGNEL----- 1363
QY 1030 PEDLKBEKIPDGLRQMFYTLGDYRDLF----- 1059
Db 1364 -DKELKEGKIIPAFILRSMFYTFGRDFLFGTDISKHGEGSKLKEQIDSLPKNGDQSP 1422
QY 1060 ----- 1059
Db 1423 NGKTRQEWMTSHSHEIMEMALCALVYIGAKKDDFTENYGYNNVKSXTLLEBPAPQ 1482
QY 1060 ----- 1059
Db 1483 FLRWLTWYDYCYTRQKYLKDVQEKCKSNDQKCDTECNKKCEDYVYKMKKKKWIPOD 1542
QY 1060 -----SGSNDT-----TSVKDTPSSN----- 1077
Db 1543 KYKQDBRDKRFRQHGIGVMVTDYGTNATDYLNKFKTASCGDKGSASVVOBRIQLLEK 1602
QY 1078 -----DNLKXIV 1084
Db 1603 QAYYADAKHCGCTFEIENDKYTNISXDKCKGLVEANTGAIKQNGKPNVNNLKELT 1662
QY 1085 -----LLASGSTE-----OEREXM 1098
Db 1663 EDVLFPSRLRICFHALDGNVTDPEYKOBNGILRKRLMEVAATEGNLQOYKEKKEKXI 1722
QY 1099 -----NKY-----KEIKNFRKCTERS 1115
Db 1723 KTSDAHKYSYEVPCSAMKYSFYDLRDIILGIDNLEDEKQTEBMLKKI PNNNGTSVGKG 1782
QY 1116 APNLVSHP-----QTMENNGKIYHGWYCAL----- 1142
Db 1783 SDSTTGNPQSTARKEFFENKECVNNAMICGYKGRDGNSSGARSDEDLKCKGSPSD 1842
QY 1143 ----- 1142
Db 1843 DDYPMGKNDBGTAYOFLRMFAWGBDFCKHKEKELKLVGACNDYTCGDNEBKAKKCTD 1902

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QY 1143 -----TSKDKI-----AKGE----- 1153
Db 1903 ACTQYKKFISEMKQYQEKQIKKYGENDKIYSEHPVAKDAEAYLDQKKI CENKSG 1962
QY 1154 ----- 1153
Db 1963 DCEYCKMADVSTQRLTDGNSQNMPPASLDDEPKVEGKNCQVPRGPRVARETPSPVSL 2022
QY 1154 -----KKPOKLEN----- 1161
Db 2023 ISKATASKEAKTAPPTQPKVLENLTTEBRAQOTRRRAAQOTRKRTSTATTTESDVGM 2082
QY 1162 -----PENLDEANKKX-----PQ-----YQYT 1181
Db 2083 VKAILSNKPPSRGGIEGCKPRTYQGPYKWCIGVSKXENENGICMPRRRKLCTINIOYL 2142
QY 1182 NVKLD-----EN--SGTSPRTQ----- 1197
Db 2143 NYETENKRDNDIEAFIKCAIETQFLMLKTIENPAENELONGTIPDEFKRLMYTYG 2202
QY 1198 -----TOASSD-----NTPPT----- 1208
Db 2203 DYKMPFGTDISNDKIIITVNSVTTLNENKKQDKKXDEBLKIFMEKNKKFIWGM 2262
QY 1209 -----LTHPYKRPITYPRWFEBMGESFCREKXR 1236
Db 2263 IYGLTYHLTDENEKEKIRDYQYNDMTKLTPLSEFPVKRQFLMFTWMAEFPCKRQ 2322
QY 1237 IKQIKVDQKVE--NGDVGRSGDGEACDSISTHDYSTVPSFNCGCKHSGSYKRWIERK 1294
Db 2323 LKLEBACKEVECNQ-----SNDKTOE-----CAEACTYONFPIKXW 2360
QY 1295 KIEFHQSNAYGQ-----OKTDATNNGNTFDKEPC----- 1325
Db 2361 KTEYERQREKFKKODKQKYYKDYPTERDIEKACAEHYLMKLELQGNKDCMQKPS 2420
QY 1326 -----KLETWPD----- 1333
Db 2421 SOLPKTQOSQSDANDMPESLDYVPBEFNCBCEPBLSKGSMITHKTEPKI PNNCVE 2480
QY 1334 -AAKFLER-----LKNRPCNTKNEYGD----- 1355
Db 2481 KAAAYLSKEANNDITLKEKFTPIBSTEKESKSTNNNFCDPKPYAPDKYIGRRNP 2540
QY 1356 -----DIDFE-----KDSKTFQHTK--YGPCKPRTKNGCQNGCVGLNGCDG-- 1398
Db 2541 CENREBNRPKYVDYMKCYKNSKFQEKRVCP--PREHMCILR-----NLDEIKI 2589
QY 1399 DKSIDAKEIAKM-----RSSITDVVWRY--SPN-----DTNFBGDDLKDAQOHAN-- 1442
Db 2590 ERLDQSNYLLKQVARTARNEGIDIIKNFNSBNGCAMPICDTMKYSFADIGDIVRGDML 2649
QY 1443 -----IFPGI-----RKQWMCYVCG 1459
Db 2650 RIGGYLPPVEYIKLYVEYIIGKRRANKKGNKYNDOVTPRSAMWANDRNDIMK--AMTCK 2708
QY 1460 VDICQOTNINERTDGE--YIQIRALFK-----RWVENF-----LEDY 1495
Db 2709 APEDAKLFRKGRMDGFERITLIDQKCHKODRPVDDYIPQFRFWMTSEYCCALMBEL 2768
QY 1496 NKINDKISHCTKKEGSKCINGCEKN--SKLEWIEKK--IAWENI-----KGRFNDQY 1547
Db 2769 EKFPKSCDHQ--KTSPRCRKNDYENKCEQCKTQCEKYNFVLMKSLFDIOSNKYELY 2825
QY 1548 ENKOOPDYNVKSI--LEBELPKIAVNDONVYIKLVF--ENGSGCTLLSNTQNNKEN- 1601
Db 2826 E--QPIYTKISTYDHYQNFQOKLKTRESCEVSVPSEYILHETSKLANYKRENDGSSNI 2882
QY 1602 -----DAIDCMLKGLGVKAKNCPKSPSGEKQSDCKPPL--PDEEDON- 1643
Db 2883 RTYAFEBTPKSYKACSGCTLPSPKN--PLDNC--PTDQKQDCKELQFTFCSKNDYDNL 2938
QY 1644 -----PEBNTLEPPK--FCP--PTQPPREBK-----GETC 1670

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Db 2939 DNMAVLYLNSDDKGVLIIPRRRHLCRPTTAVNYRKGDEILKCKLLTSAPSGQL 2998
Qy 1671 GNKEKKE-----KK--ESES----- 1686
Db 2999 GQKYSEBELCPKAMKYSYADYDIIKGTDMWDTLSSEKIKKIFETSSEATENRKTMBN 3058
Qy 1667 -----PAKESG-----PAEPAPFASE 1706
Db 3059 NRRQIWMHMLCGYKATSKVTILDEGMCOLEKDEETNOFLRWLEWAKACCKKKVSDSL 3118
Qy 1707 ET-----ETNPP-----EPPG----- 1717
Db 3119 KTKCRSMEDNFEASELLRQPCQNDIRKYSILNLIKNTMENLIKVKQLKQSSGND 3178
Qy 1718 -----TGPAAPPTPAPPT----- 1731
Db 3179 NKPSHENQYIKSKDSQCALELNDINEIVGTCKNNENNEFKVLKCLYGLYFVEDETH 3238
Qy 1732 -----PDTPLRPOA-----DEPFDST-----ILQTTIPGV 1759
Db 3239 KKHVLIDGNIKKEEQVRPQALYFTTPHYDSFYQAPLFSTHRYAQYDPRKNDILKSSISVVI 3298
Qy 1760 ALALGSIAPLFELKKTAKAVGNLFQILQIPKSDYDIPTLKSSNRYIPIVSDRYKGTIY 1819
Db 3299 VSALGLILHFKKKFKSV--DLNLIINIPOGEYGMPTLESKNRIYIPRSGPYKGTIY 3357
Qy 1820 MEGDS--DEKKAEMSDTTDVTSSESEYELDINDIYVPGSPRYKTLIEVLEPSCNNT 1877
Db 3358 MEGDTSGEDGKWMYDLSSDITSSSEYELDINDIYVPGSPRYKTLIEVLEPSCRP 3417
Qy 1878 ASGNKTPBDTNDIONDGIPSSKIDNEMNOLKKEFISNMLON--OPNDVPNDYTSNGSST 1936
Db 3418 SD--DTPS-----NDTPRTNRFIDDEWELKHPVSOYLPTNPN--NNYKADIPM 3465
Qy 1937 NTNITTRHVNNTNTTMSHRNMEENLLPSIHDGNYLSEGEYSYVNM--VNSMNDIP 1995
Db 3466 NTE-----PNTLYSDNPEKPKFISIHDRDLYTCKEISYININSTNNNDIP 3512
Qy 1996 INRDNNVSGIDLINDSL 2013
Db 3513 MNAARDSYRGIDLINDSL 3530

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1PMDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-153-273-10
Query Match 11.4%; Score 1385; DB 4; Length 700;
Best Local Similarity 40.8%; Pred. No. 2.3e-63;
Matches 328; Conservative 106; Mismatches 207; Indels 162; Gaps 34;
Qy 113 CAPRRHLCKNKPNNNSNDSSKAKDLAEVCAARYEGESIKTHYPKYDSKPGSDF 172
Db 10 CAPYRLHLCY---NLESIDTSTHKLLEVCMAAYEGNSINTHYQRTNEDSAS 66
Qy 173 PMCTMLASPADIGIINGRDLTYG--NKKKKONKTEPERKEIRKIH-DLTK 229
Db 67 QLTVALASFADIGIYVGDLYGDKYKEXQ-----RKLLEQLKDIFFKIKHDKVWK 120
Qy 230 DEKQKRYNGD--EDNFKYKLREDWMTANRETVMGAMTCSKEIDNSSYFATCNDTGOGPS 288
Db 121 TNGQDERIYIDAKGDPFQLREDWMTSNREYVMALICHAPREANYFIKTACN--VGKK-- 177
Qy 289 QTHNKCRCDDKQGANAGKPKAGDGVTVIPTYFDVVPQYLFMFEEWADFCRKKKKKLEN 348
Db 178 -TNGQCHC-----IGGD-----VPTYFDVVPQYLFMFEEWADFCRKKKKKLEN 220
Qy 349 LEKQCRGKDSDEIRYCSRNGYDCEQTSIRKGYKRMGCTDPCFACSGSYEMWINDQKQ 408
Db 221 LQKQCRDYEN---LYCSGNGYDCTKTIYKKGKLVIGHCCTNCSYWCMTYETWIDNKKKE 277
Qy 409 FDKQK--KYTKELISDQCG-----RKKRAVGTTTYE--GYEKSFEKLRNDGYGVDAFAG 460
Db 278 FLKQKRTETELISGGSGSKSPKRTYKRAARSSSSSDNNGIESKFKLKEVGIQDYDKELK 337
Qy 461 LLNNEKACKDITDGGKINPKFKNVSGGAVVGGSGGTSAGSTNDENKGTFRSEYQPCP 520
Db 338 ILNKEGICQKQPOVG--NEKADN-----VDFTEKXYVTFSTETICEBCP 380
Qy 521 DCGVQHKGNQWERTKYKQRKMSKLYPIINGKAVLLKSLKLVYVDMMLIKKNWKEPCLT 580
Db 391 WCGLE--KGGPPW--KVKGDKTCGSAKTTYPKNTITDIPVLYPDSQONILKKNYFC-- 435
Qy 581 QNSSDGVSQVVTYGASGNGSEKELVDEMKCYKANEVQKVNVOGEVEEDDELGAGGL 640
Db 436 -----EKGAPEGGQIKK-----WCYI-----DEHR----- 456
Qy 641 CILPNPKKKEVSEAK-----SQNNHADIQKTFHDFPYVVAHMLKDSIHMRTKRLKSCI- 695
Db 457 ---PSSKNNNNCVGEMDKFTQKQT--VKSYNVFEFMDVMDMLHDSVEMKTE--LSKICIN 510
Qy 696 ---SNGKTKKNGCNKKKDCFEKRVKQKETEMKPIKHFKTQEGI-----PBGVY 743
Db 511 NNTGNTCTRNKKCKTCDGCFQKWKVEKKQOEMWAIKHFGKQTDIVQOKGLIVSPYV-- 568
Qy 744 FTTLELILK----LQFLKEDTEENTENSLDAEBAELKGLQIKLLENNMLAVVNACTE 799

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Db      569  --VLIDLVLKGNLQNIK-DVHGDT-----DDIGHIKLT--LDEBDVAVVLAGKD 614
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Db      615  NTTI-DKLQHEKEQAEQCKQKECECKKAAQESKGRSAETREBERTQPADSAGEVEE 673
Qy      847  EKEDDENEDDEDEVRDEETAK 869
Db      674  EDDDDYDEDDDDVVDVVDVSE 696

RESULT 4
US-10-153-273-8
; Sequence 8, Application US/10153273
; Publication No. US20020169305A1
; GENERAL INFORMATION:
; APPLICANT: Slim, Kim L.
;             Chitnise, Chetan
;             Miller, Louis H.
;             Peterson, David S.
;             Su, Xin-zhaun
;             Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
;                   AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobe Martens Olson & Bear
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,273
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FMDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-153-273-8

Query Match      5.8%; Score 702; DB 4; Length 921;
Best Local Similarity 26.2%; Pred. No. 8.5e-28;
Matches 237; Conservative 131; Mismatches 346; Indels 192; Gaps 28;
Qy      1337  FLERLKGCKTKNKEGGDIDPEKSKTFQHTVEYCGPCKPFTNONGNCG-----VSG 1391
Db      12  FLNLSKSGPCKDNDNAEDNIDFGDKTFKADNCKPQSQFTVDCNKGDTGKCKNG 71

```

```

Qy      1392  LKNGCGDKSIDAKEIAKMSSTTDVVMKVSNDNTNFEQDGLKDAQOHANIFKGIKDV 1451
Db      72  SNGKKNQNDVITYTASDINNGNSIGNIDMVSDKANFNG---LDACGANIFGIRKEQ 128
Qy      1452  MKGCVGVGVDICEGTNINER--TDGEYIQRALFKSVENFLBDYNNKINDIKSHCIKKG 1509
Db      129  MKCAKVGGLDVCGLNKNGNSIDKQKQIIRALLKKNVEFFLEDYNNKINKINIKSHCIK 188
Qy      1510  EGSKINCCEKNSKLEKWIIEKKIAEWENIKGRENDQYENKQPDYNNYSILBELLIPKIA 1569
Db      189  NESTCTNDCKPKCTCVSEWINQKRTWKNIKGHYKTQENEGDN---NMKSLVTIDILGALQ 245
Qy      1570  VVNDQNVIKLC---VFENKGGCTLSNTQ--NNKENDALDCLVKLVGAKKCPGPS 1623
Db      246  PQSDVNNKAIKPCSGLTAFESFCGLMGADNSKEKEGEDVLCLMLKLEKIQCK-KKH 304
Qy      1624  GEK--QSDCKEPPPLPD---BEDQNPENLTLEPPKFCPTTPPEBKGETCGNKEEKD 1678
Db      305  GETSVENKGSCTLDNTLTLEBPILBENQVEAINIC-----KQTVED 348
Qy      1679  EKKESEBEPAKESGPAABEPAPTAESEETETNPEPPGTGPAAPPTAPPTDTPPP- 1737
Db      349  KKEKEBEETC-----TPASPVBEKVPVH 371
Qy      1738  -----LRPADPEPDSITTIQTTPRGVALALGSIAPFLKXKTKASVGNLFOIQLPK 1790
Db      372  VAWRRTFTPEVPFKIMGRNRKTCET-----VAEMLKDKKGRITVGCYR---K 418
Qy      1791  SDYIPIFLKS---NRYIPVSDRYKGTIYMS--GDSDEDKYAFMSDITVT----- 1839
Db      419  ETYSWTDESKIKMGHGACIPPRQQLCHYEKIMTNNELKNAFIKCAAAETFLW 478
Qy      1840  -----SSESEYELD--INDIYVPSPPRYKTLIEVLVPSGNNTTASGKNTPSDTRNDIQ 1892
Db      479  QNYKDKKGNABEDLDEKLGKGIIPEDFRQMFY-----TFADYRIDCL 521
Qy      1893  NDGIPSSKITTNENQLKKEF-----ISNMLQNP-----DVPNDYTS 1931
Db      522  GTDISSKDKTSGVGVKVCNIDVFYKISIRYKKSWEETNGVPYIWEGLCALSYDTSL 581
Qy      1932  GNSSTNTNITTSRHN-----VDNNTNTTMSRDMEENLLPSIHQNLYSGBEYSYV 1985
Db      582  NNVAPEYHKULTTEGNNEKVIPIGSDSTTISKPSERQFLRWLTWEENCKQKXKYY 641
Qy      1986  NMVNSMNDIPINRDN-----NVYSGIDLINDSLGGKPIIDYDEVLKRX 2029
Db      642  VLAACKCDVDYDGKCKGKGCVAACKQCKQYHSMWIGIWDYKKQKGRYTEVKKIPLYKE 701
Qy      2030  ENELFGTEYTK---RTSTQNVAKTNSDPINQLELPHKMLDRHRDMCEKKNK-----ED 2082
Db      702  DKDVKNSDADLDYLTQLONNKCVNGTTDENCEYKCMHTSSTNSDMPESLDEKPEKYKD 761
Qy      2083  ILNKLKEEMNKENINSKGTYSNDKPSHNHVLANTDVISIQIDMDNPKTKNETTNDTNOQ 2142
Db      762  KNCVCVNECNALSVSGSG---FPDQAGFGGVLVBETCK---GLGPKKKIIBPYQVDPIND 815
Qy      2143  --KSTM 2146
Db      816  ILKSTI 821

RESULT 5
US-10-087-013-10
; Sequence 10, Application US/10087013
; Publication No. US20040062769A1
; GENERAL INFORMATION:
; APPLICANT: Arthur Scherf
; APPLICANT: Louis H. Miller
; APPLICANT: Benoit Gamain
; APPLICANT: Drot I. Baruch
; APPLICANT: Pierre Buffet
; APPLICANT: Christine Scheidig
; APPLICANT: Jurg Gysin

```

```

; APPLICANT: Bruno Pouvelle
; APPLICANT: No. US20040062769A1utaka Fujii
; APPLICANT: Joseph Smith
; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; TITLE OF INVENTION: (PFEMP1) THAT MEDIATES ADHESION TO CHONDROITIN SULFATE A
; FILE REFERENCE: NIH176.001C1
; CURRENT APPLICATION NUMBER: US/10/087.013
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/24195
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,023
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
; US-10-087-013-10

```

Query Match 3.7%; Score 445; DB 4; Length 311;

Best Local Similarity 27.7%; Pred. No. 4,5e-15;

Matches 122; Conservative 61; Mismatches 120; Indels 138; Gaps 17;

```

QY 902 DACSLKY-GGNNSRLGRCVTPSGEPTTSSDKGALICVPRRRRLYIKIYDMATKTESP 960
DB 6 DGCNOKYAGKDKYPGWDC-----NSQIHHTHNGA-CMPRRRQKLCVSGL-----TKTDRI 55
QY 961 QASGEASSTSGSTTPPSKEALLKAFVESALIEFTFLMHRKYKEEKKAVAQAGHGLPR 1020
DB 56 KAI-----EYIRTEFIKSAIETFLMHRKYKEEKKAVAQAGHGLPR 85
QY 1021 VEEGSPEDYDPEDKLEKGIKPGFLRQMFYTLGDRDILFSGSNDTS-VSKDTPSSNDN 1079
DB 86 -----EAEAELEKNGNIPEGFKQMYTFGDRDIFEGGRDISTHAYISGSP----- 131
QY 1080 LKNTVILLASGSTGEQREKQNYKEIKNFKCSTERSAANLVSHPTWENNKKYIWHGM 1139
DB 132 -KVITILEKENDAKYAAKQNSNNELD-----DWDQHGKDWEGML 172
QY 1140 CALTSKDKIAKGVKKPQKIEINPENLMDANKKPPQOYQYTNVCLDENGSTSPRTTQ 1199
DB 173 CALTHK-----ISDEKKKEIKNKYSYK-KLNE-----SPKGS--- 204
QY 1200 ASSDNTPTTLTHFVKRPTFYFRMFEWGESFCERKKRLKQIKVDCKVENGVGRCSDGE 1259
DB 205 -----NKVEDFAKPPQFLRMFIEWGDEFCAQREKEAKYVSCS-----DAKDYD 249
QY 1260 ACDLSITHDYSTVSPFCGCGKCSYRKMIERKKIEFHQSNAYGQOKTDATRNAGNT 1319
DB 250 GCKKTKSN-----ASCVSACKVEYDIYTKKQVEYTKQKGFDAKIT----- 291
QY 1320 FDKPCKTLETWPDAAKFLER 1340
DB 292 -DKEGYEGFST-KDASEYTKK 310

```

RESULT 6

US-10-087-013-8

; Sequence 8, Application US/10087013

; Publication No. US20040062769A1

; GENERAL INFORMATION:

; APPLICANT: Arthur Scherf

; APPLICANT: Louis H. Miller

; APPLICANT: Benoit Gamain

; APPLICANT: Doro I. Baruch

; APPLICANT: Pierre Buffet

; APPLICANT: Christine Scheidig

; APPLICANT: Jurg Gysin

; APPLICANT: Bruno Pouvelle

; APPLICANT: No. US20040062769A1utaka Fujii

; APPLICANT: Joseph Smith

```

; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; TITLE OF INVENTION: (PFEMP1) THAT MEDIATES ADHESION TO CHONDROITIN SULFATE A
; FILE REFERENCE: NIH176.001C1
; CURRENT APPLICATION NUMBER: US/10/087.013
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/24195
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,023
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
; US-10-087-013-8

```

Query Match 3.6%; Score 439.5; DB 4; Length 407;

Best Local Similarity 29.3%; Pred. No. 1.2e-14;

Matches 145; Conservative 56; Mismatches 133; Indels 161; Gaps 24;

```

QY 895 KDNESLDACSLK-YGGNNSRLGRCVTPSGEPTTSSDK-----NGAICVPRRRRLYI-- 947
DB 3 QDGTFKIIECCTKYPTKNDYPGWNC-----TDKVINREBSCMPRRRQKLCIHN 52
QY 948 -KTIYDQATKTESQASGEASSTSGSTTPPSKEALLKAFVESALIEFTFLMHRKYKEEK 1006
DB 53 LEHLSERATETE-----LRKAFIECAIETFLMHRKYKEEK 88
QY 1007 KAVAAQ-EGAGHGLPRVEGSPEDYDPEDKLEKGIKPGFLRQMFYTLGDRDILFSGSNDT 1065
DB 89 KDEKKTBECC-----ISDDPD-DPQKLEGGTIPEDFKQMFYTLGDRDILFSGSNDT 136
QY 1066 TSVSKDTPSSSDNKLKQIVILLASGSTGEQREKQNYKEIKNFKCSTERSAANLVSHPT 1135
DB 137 TDISKGHKES-----ALG-----KKIDSLFKNGDQKSPSG--KTPTPE 172
QY 1126 WENNKGKIYHGMVLCALTSKDKIAKGVKKPQKIEINPENLMDANKKPPQOYQYTNVCL 1185
DB 173 WMDNYGPDIMGMVCGLS--HHKNGKKEQLRK-----NLTD--NNK-----YTKIS- 215
QY 1186 DENGSTPRTQTQOASDNTPTTLTHFVKRPTFYFRMFEWGESFCERKKRLKQIKVDCK 1244
DB 216 -----SKLEDFASRQFLRMFIEWGDEFCAQREKEAKYVSCS-----YTKIS- 254
QY 1245 KVENGDVGRSGDEADCSISTHDYSTVSPFCGCGKCSYRKMIERKKIEFHQSNAYGQOK 1304
DB 255 EYECG--SQENGKKEACNA-----CEAYSWLKDMDQYEQGTAK 293
QY 1305 YGQOKTDATRNAGNTFDKPEFKTLETWPDAA-----KFL-ERLKGKPKTKKKEVGDDID 1358
DB 294 FDKDKK-----DKKFDGTSAEVDVAASVSHVLELQELKXNLCTK-----GDCAC 337
QY 1359 FEKDKTPQHTTEYCG 1373
DB 338 MEKPSAQDETEELG 352

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RESULT 7

US-10-087-013-7

; Sequence 7, Application US/10087013

; Publication No. US20040062769A1

; GENERAL INFORMATION:

; APPLICANT: Arthur Scherf

; APPLICANT: Louis H. Miller

; APPLICANT: Benoit Gamain

; APPLICANT: Doro I. Baruch

; APPLICANT: Pierre Buffet

; APPLICANT: Christine Scheidig

; APPLICANT: Jurg Gysin

; APPLICANT: Bruno Pouvelle

; APPLICANT: No. US20040062769A1utaka Fujii

```

; APPLICANT: Joseph Smith
; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; TITLE OF INVENTION: (PFEPM1) THAT MEDIATES ADHESION TO CHONDROITIN SULFATE A
; FILE REFERENCE: NIH176.001C1
; CURRENT APPLICATION NUMBER: US/10/087.013
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/24195
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,023
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
; US-10-087-013-7

```

Query Match 3.5%; Score 422; DB 4; Length 294;

Best Local Similarity 26.9%; Pred. No. 6,6e-14;

Matches 115; Conservative 56; Mismatches 105; Indels 152; Gaps 17;

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QY 895 KDNESLQDASLKYGNNSRLGMRCTVPSGEPTSSDKNQAI CVPRRRLYYKKI -VDM 953
DB 5 KNSGSI-DNCNAK--NRKKNEMQC-----DKNTEVDGNBEGVCMPPRRKSCICIHNLTLRE 55
QY 954 ATKTESPQASGEASSTSGSTTPPSKALILKAFVESAIEFPFLMHRYYKEKKAVAG 1013
DB 56 QYK-----NKYQLREAFYKCAKENTNLMDKTKDKN----- 87
QY 1014 AGHGLPRVEEGSPEDYDPEDLKEGKI PDGFLRQMFYTLGDYRDLFGSNDTTSVSKDP 1073
DB 88 -----EABELAKKGKIPEDFMKIMVYTFGDFRD--FCLEND--MGKQVD 127
QY 1074 SSSNDLNKIVLLASGSTEOERKMKYKEIKNFKCSTERSAPNLVSHPTWMENNGKY 1133
DB 128 KVK---KNINKVFNNSSK-----RGFKKID-----PENMMNENGPO 160
QY 1134 IMHGVNLCALTSKDKIAKVEKKPKQKIEPNENLMDANKKPKPOYQYTNV-----KLDDNS 1189
DB 161 IWMGMICALIHAD-----TKDSIKKNDN-----YKYEKVTILLARDGDN 199
QY 1190 GTSPTTQOASSDNTPTTLTHFVKRPTFYRWFEEWGESFCRERKKRLKQIKVDCKVENG 1249
DB 200 G-----MTLSEFAKKPKRLKMFVEMYDYCKERQKYLTEVASTCKSIDG 243
QY 1250 DVGRCSGDGEACDSISTHDYSTVPSFNCPCGCGKHCSSYRKMIERKKIEFHQSNAYGQK 1309
DB 244 GQLKCD-----RGCNKNCDEYKKYMRKKKEEWNLQDKXY----- 277
QY 1310 TDATRNNG 1317
DB 278 KDKRENG 285

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RESULT 8

US-09-924-154-13

Sequence 13, Application US/09924154

Patent No. US20020127241A1

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use

FILE REFERENCE: 05213-0465 43170-262105

CURRENT APPLICATION NUMBER: US/09/924,154

PRIOR FILING DATE: 2001-08-07

PRIOR APPLICATION NUMBER: US 60/223,525

PRIOR FILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13

LENGTH: 1421

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; TYPE: PRT
; ORGANISM: Mammalian
; US-09-924-154-13

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Query Match 3.5%; Score 421.5; DB 3; Length 1421;

Best Local Similarity 18.0%; Pred. No. 5.1e-13;

Matches 348; Conservative 272; Mismatches 558; Indels 755; Gaps 90;

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QY 392 FFACSGYENMIDNQRKQFDKQKYTKKEISDGGKRRKAVAGTTKYEGYKSYEK----L 447
DB 17 YFAKARNEYDIKENEKFLDYKKEKFNELD-----KKKYGVNQYTDKKIFFIENKLDIL 70
QY 448 KND-----GYGT--VDAFLGL--NNBKAKDITDGGKINFKVNSGGVVGGS-- 492
DB 71 NNSKFNKRWKSYGTPDNIDKMSLJINGNHEMENN-----NYQSFLLSTSLIKONKY 123
QY 493 -----SOGTSGASGTNENKGT FYRSEYQCPGCPGVQHKGNQWERTKYKRWMS 544
DB 124 VPINAVRSLRSLFLDRIRNGRTSSNVEVLSNCR-----EKKRGMKWDCKKNDRSNYV 179
QY 545 KLYRPNKQWVLLKSLKLVK-----DMMILKKN-----WKEFLTLQN 582
DB 180 CI---PDRITQLCVNLSIITKYTKETMKOHFIASKESQLIKDKDNKYSKFCNDLK 236
QY 583 SSDGSVGSVVTGAS--GNSKEKELIDEMKCYGNHGVQKYNQGVYEBDDDELKAGGL 640
DB 237 NSFLDYGLHLMGNDMDRGYSTKAE-----NKIQEV-----FKGAHG- 273
QY 641 CILPNPKKNKVEBAKSONNHADIQKTFHDFPYVVAHMLKDSIH----- 685
DB 274 -----EISEHKIKNFKKMMNFRBKLMBALMSEHNNINNCNIPQBELQITQW 323
QY 686 ---W-----RTRLKSCISDGKTKCRN-----GCNKKC--DC--FEKRVQKET 723
DB 324 IKENHGEFLERDRSKLPKS-----KCKNNTLYEACKEKCIDCMKTRDIIIRSKF 375
QY 724 EWKPIKDHFKQEGIP--EGYFTLLEILKQFLKEPDEEN--TENSIDAEAE--EL 776
DB 376 EWHTLSEKEYEYOK--VPKENAENY-----LTKISENKNDAKVSILLNCAEYSKYCDC 427
QY 777 KHLQKILLENBNLVAVNAGTBOKTLMKDLNLHENDATK--CKDCPLPREDKSRGSA 834
DB 428 KHTTLTVK-----SVLNG--NDNTIKEKEHIDLDDPSFGC----- 462
QY 835 DPSPDIFIPREKEDDENEDDDEVRADDETAKEETGSAITDTTSLDVCPIVKYLT 894
DB 463 -----DGN-----SVDTNTKVMCKCKPKYKLT 484
QY 895 KDNESLQDASLKYGNNSRLGMRCTVPSGEPTSSDKNQAI CVPRRR-----RLY 946
DB 485 KD-----VCVPRRQELCLGINDRIY 505
QY 947 IKKIVDMATKTESPQASGEASSTSGSTTPPSKALILKAFVESAII-ETFFLMHRYKES 1005
DB 506 DKNLNL-----MIKEHILALAIYESRLIKRYKOK 534
QY 1006 KKAVAQEGAGHGLPRVEEGSPEDYDPEDLKEGKI PDGFLRQMFYTLGDYRDLFGSNDT 1065
DB 535 -----DDK-----BYCKIINKTFADIRDI--GGTDY 559
QY 1066 TSVSKDTPSSNDLNKIVLLASGSTEOERKMKYKEIKNFKCSTERSAPNLVSHQOT 1125
DB 560 W-----NDLSNKRKLVGKINTNSNYVHRNQND--KLFR-----DE 592
QY 1126 IMENNGKYMGMVLCALTSKDKIAKVEKKPKQKIEPNENLMDANKKPKPOYQYTNVL 1185
DB 593 WMKVIKKQVMN--VLSWVFKDQTV--CKEDDIEN----- 622
QY 1186 DENSGTSPTTQOASSDNTPTTLTHFVKRPTFYRWFEEWGESFCRERKKRLKQIKVDCK 1245
DB 623 -----IQPFPMFSWGDYQCDTKMLETLVCK 653
QY 1246 VENGDVGRCSGDGEACDSISTHDYSTVPSFNCPCGCGKHCSSYRKMIERKKIEFHQSNAY 1305

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Db      654 EK-----PCBD-----NCRKNSYKEMISKKKEBYNQAOY 687
QY      1306 GQOKTDATRANGNTPEKCTLETPPAKLELKGKPGCKTKNEYGGDIDFEKDSKT 1365
Db      688 QEQY-----KGNVKNYKSEF--KSikePVYLKKTSEKSN-----LNFEDEPKE 729
QY      1366 FOHTEY-----CGPCKEKTNCQNGCGVGLNGCGGDSI---DAKEIAKORSSSTDVVM 1419
Db      730 ELHSHYKCKTKCEPEVK-----DVPISIRNNEGTSGAVPEESTETAHRTETTD--E 781
QY      1420 RVSDDTTFEGDDLDKACOHANIPKGIKDVWKGVCYVDICEQTNINERTDEKEYIO 1479
Db      782 RKNQEPAN-----KOLKN-----POQSVGE--NGTKDLLO 809
QY      1480 IRALFKRVENFLEDYKNKINDISHCICKEGSKCINGCEKNSCKLEKTEKIAEWENI 1539
Db      810 EDLGSRSDEVTQEFQ-----VNHGIPKGE-----DQTLGK----- 841
QY      1540 KKRFDYQENKQDPYVY-----KSLBELIPKIAVNDQNVYKICVENSCKTLLISNT 1595
Db      842 -----SDALPNIGEPETGISTTEESRHEGHNQALSTSVDE-----DELSDT 884
QY      1596 -----ONNKENDADICMLKGLGVKAKNCPKSGEKQSDCKEPPPLPDEEDQNPENTLEP 1651
Db      885 LQHEDTYKEND-----KLPLESSTIT--SPTESSSDTEETPIS-----EG 924
QY      1652 PKFCPTPTQPEPEKGETCGNKEEKKDEKESSEPAKESGPAEAPAESEETETN 1711
Db      925 PK-----GNEQKRDD-----DELSTKISVSP--ENSRPERTADOT--SN 959
QY      1712 FPEEPGTPAPAPSTPAPPTPTPTPLAPRAD-----EPD-----STLQTTI 1755
Db      960 LKKGADVDIMPKAVIGSSPDNINVTGQGNISGVNSKPLSDVDPDKNHEEVEKTS 1019
QY      1756 PFGVALAGSIAFLFKKKTAKSVONLFOILOIPKSDYDIPLKSSNRYIPIVSDRYGK 1815
Db      1020 NSDNVQOGSGIYNNVNEKELKDTLEN-----PSSSLD-----BGK 1054
QY      1816 TYIYMEG--DSEDEKVAFMSDT--TDVTSESEYEELDINDIYVPSPKYKTLI----- 1865
Db      1055 AHEBELSEPNLSSDQD-----MSVTPGLDNTSEET--ERISNNEYKVNREGERLTKEYE 1109
QY      1866 EYVLEPSSGNTTASG---KATPSDTRNDIQNDGIPSSKITDNEMOQLKEEISMTLQNO 1921
Db      1110 DIVAKSHNRRESDDDELVDENSDELSTVNDSEDA--EAKMKGND-----TSEMSHNS 1159
QY      1922 PNDVNDYTSGNSSSTNTNITTSRHNVDNNTYTMSRNMENELLPSIHQNLVSGREY 1981
Db      1160 SOHIESDQOKDMKTVGDLGT--HYQVEISVPVTEIDEK--LRSEKSKHKAEE 1213
QY      1982 SYNVMNVMSNDIPINRDNVYSGIDLINDSLSGKPIYIDVELKREKNEELFGETNKR 2041
Db      1214 RLSTHTDIKIN--PEDRNSNTLHKDINRNE-----ENBRH 1246
QY      2042 TSTQNV-----AKTNSDPJHNOLELPHKWLDRHRDMCEKMKKNDIANK 2086
Db      1247 LTNQININISOERDLOKHGFHTMANLHGDGVSERSQINH--SHHGNDRODROGNSGVILNM 1303
QY      2087 LKEENKKNINNSGKTVNSDNKPSHNHVLNTDVSIOIDMDNPKTKNEELTNMDTNDOKSMT 2146
Db      1304 RS--NNNNFNPIBRYNLYDK-----KLDIDLVEKNDSTYELIKKLAIEI 1347
QY      2147 DTIIDLLE-KYND 2158
Db      1348 NKCENEISVRYCD 1360

```

RESULT 9
 US-10-153-273-4
 ; Sequence 4, Application US/10153273
 ; Publication No. US20020169305A1
 ; GENERAL INFORMATION:

```

APPLICANT: Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Kim-zhaun
Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FMDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-153-273-4
Query Match 3.5%; Score 418; DB 4; Length 1435;
Best Local Similarity 17.4%; Pred. No. 7.9e-13;
Matches 337; Conservative 259; Mismatches 555; Indels 782; Gaps 85;
QY 392 PFACGSYENWIDNRKQFQKQKTYKEISDGGKRAVGGTYYKEGYEYSFYK---L 447
Db 17 YFARARNYDIKENKEKPLDYKKEKNEELD-----KKYGVNQTKDKKIFPIENKLDIL 70
QY 448 KND-----GYGT--VDATFLGL--NNEKACDITDGGKINPKVNSGGGVGCG-- 492
Db 71 NNSKFNKRWKSYGPPNDIKNMSLINKANNEMFNN-----NYQSLSTSSSLKONKY 123
QY 493 -----SGGTSGASGTNDENKGFYRSVEYCCOPPCDGVQHKGGNQMERKTKYVKRMS 544
Db 124 VPINAARVSRILSLPDSKINNGRNTSSNNEVLSNCR---EKKGKMKDKCKKANDRSNYV 179
QY 545 KLYRKINGKAVLLKSLKRVK-----DMAILKCN--WKEFCLTQN 582
Db 180 CI---PDRRIQICIVNISIIKTYKETWKDHFIEASKESQLLKKNDKNKYSKFCNDLK 236
QY 583 SSDGSVGSVTTGAS--GENSEKEKELIDEMKCYKGNVQKYNVQGVVEDEDELKAGGL 640
Db 237 NSFLDYGHILANGNDMDFGYSYTKAE-----NKIQEV-----FKGAHG-- 273
QY 641 CILPNPKKKEVSEAKSQNNHADIQKTFHDPFYVVAHMLKDSIH----- 685

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Db 274 -----EISEHKIKFRKEMWNEBFEKLMWAMLSSEHKONJINNCNINPOEELQITOW 323
Qy 686 ---W-----RTERKSCISIDGKTMKCRN-----GCKKC--DC--PEKVVYKOKET 723
Db 324 IKEMWGEFLERDNNKLPKS-----KCKNNTLYACEKEKCLDPCMKRYDMIRSKF 375
Qy 724 EWPXIKDHFKTQOBGP-----EGYFPTTLELILKLOFLKEDTEEN-TENSLEAEAE--EL 776
Db 376 EMTHTLSKEVETOK-VPKENAEWY-----LIKISENNDAKAVSLILNNCDAEYSKJCDC 427
Qy 777 KHLKILKLENNENLAVNAGTBOCTLMDKLNEHLNATK--CQDCPLPEEDSRGSA 834
Db 428 KHTTLVYK-----SVLNG--NDMTIKKEKHIDLDPSKFGC-----462
Qy 835 DPSPIFIPREBEKEDDENEDDBVARDDEBTAKETTESADTSTSLDVCPIVGYLT 894
Db 463 -----DKN-----SVDNTNIV-----473
Qy 895 KDNESLQDASLKYGNNRSLQWRCVTPSGEPTTSSDKGALCVPRRR-----RLY 946
Db 474 -----WEC-----KNPYILSTKD--VCVPRRQELCLGNIDRILY 505
Qy 947 IKKIVDMATKTESPOASGSEASSTGCTTPPDSKALIKAFVESAAI-ETFFLMHRYKEE 1005
Db 506 DKNL-----MIKEHILALAIYESRILKRYKXNK 534
Qy 1006 KKAVALQAGHGLPRVEBGSPEYDEBDKLBGKI DGLRQWFFYLGDYRILFSGSMDT 1065
Db 535 -----DDK-----EVCKIINKTPIADRIDIT--GGIDY 559
Qy 1066 TSVSKDTPSSNDNLKNIVLASGTEOERKNKYKEIKNFKCSTERSAPNLVSHQOT 1125
Db 560 W-----NDLSNRKLVGKINTNSKYVHRNK-KQDKLFR-----DE 592
Qy 1126 WENNGKTIWGMVCAITSKDKIANGVEKKPOKIKENPENLWDEANKKPPQYQYTNVYL 1185
Db 593 WKKVIKKQVWN--VISWVFKDKTV--CKEDDIR-----622
Qy 1186 DENSSTPTTQOASSDTPTTLNHFVQRPTYPRFMEBGRSFCRBRKRLKOIKVDXK 1245
Db 623 -----IPQFFMFSEMGDYQODKTKMILETKVECK 653
Qy 1246 VENGDVGRSGDEACDSISTHDYSTVPSFPCGCKHSCSYKMYIERKIEIFHKQSNAY 1305
Db 654 EK-----PEED-----NCKSKNSIKEMISKEKEYYNQAKQY 687
Qy 1306 GOQKTDATANNNGTDEKFCCTLETWPDAAKFLERLKNGPCKTNKYGDDIDFEKOSKT 1365
Db 688 QEYQ--KGNVYKMYSEF-KSIIKPEVYLKTYSEKSN-----INFEDFEKE 729
Qy 1366 FOHTY--CGPCPKFK-----TNCQNGCNGYGLNGN-----CDGKSIDA 1404
Db 730 ELHSDYKNCCTWCPEYKDVPIISIRNNEQTSQEAPEENTEJAHTETPISBGPKNQ 789
Qy 1405 KEIAXKRSSTTVNVRVSDNNTNTEFGDDLKDACQAHANFKIGIRKDV--WKGYYCGVNDI 1462
Db 790 KE-----RDDSLKISIVSPENSRPETAJOT--SNLLK-LKGVLDLSMKRVAIGSSP 839
Qy 1463 CEQTNINERTDGEYIQRALFKRWVENFLIEDYNKINDKISHCIKKGSGKICINGCEKNS 1522
Db 840 NNINIVTEQDN-----ISGV--NS 857
Qy 1523 KCLERKIEKKIEMENIKKRFNDQYENKQOPRYNVYSIIBELIPKIAVVDQNDNYKLCV 1582
Db 858 KPLSDVDRPD-----KKELEDO--NSDESEETVYN--HISKSPSINNGB-----897
Qy 1583 FENSKGCTLISNTQNKENDADID-----CMUKLGVAKNCPGSPGSEKQSDCKEPPP 1635
Db 898 -DSGSSAIVSESSSSNTGLSIDDDKNGDTFYVTOJTANTEDVIRKEMADKQEDKSG--953
Qy 1636 LPDEEDQNPENLLEBPFCPTTOPPEEK-----GGETGKKEEKQDEKKESESEPA-1688

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Db 954 -ADEERSTSE-----SLSPEKCLTDNBECSLNLNHEVEKHTSNSDNVQSG 1001
Qy 1689 -----KESSGAPEAPPAABSEETETNPPEPPGTGAAPAPSTPAAPPDTPPLRPQ 1741
Db 1002 GIVNMYVEKELKOTLENPSSSLDEGKAHEELSEBPLNSDDQMSVTPG-----1048
Qy 1742 ADEPFDSTIIQTTIPFGVALALSGIAFLPKKTKKASVGNLFOJLOJPKSDYDIPTLKSS 1801
Db 1049 --PLDNTSEETTERI-----SN 1063
Qy 1802 NRYIPYSDRYKGTIYMEGDSDEDKYAFMSDTPDYVTSSESEYELDINDIYVPGSPKY 1861
Db 1064 MEY--KMYER-----EDERTILKEVEDIVLASHMNRASDDGELY-----1100
Qy 1862 KTLIEVLEPBGNNVTASGKNTPSDTPNDIQNGDIPSSKTTDNEMQOKKEFISNMLONQ 1921
Db 1101 -----DENSDLTYNDESEDA--BAKMKGND-----TSEMHSNS 1132
Qy 1922 PNDVPNDYSGNSSTNTNITTSRHNVDNNTNTMSDNMBENLLPSIHQNLVSGREY 1981
Db 1133 SQHIESDQKXNDKMTVDLGT--HVQNEISVPTGEIDEX--LEBSKSKIHKAEE 1186
Qy 1982 SYNNMYNSMNDIPINDNNVYSGIDLINDSLGGKPIDIYDEVILKREKNELEFETENTKR 2041
Db 1187 RLSHTDIHKIN--PEDRNSNTLHKDIRNE-----ENERH 1219
Qy 2042 TSTQNV-----AKTNSDPPIHOLELPHKMLDRHRDCEKMKKEDILNK 2086
Db 1220 LTQONINISGRDLOKGFHTMNMILHGDGVESRQINH--SHHGNRQDRGNSGNVILNM 1276
Qy 2087 LKEMNKENINSGKTYNSDKPSPSHNVLTNDVSIQIDMDQPKTKNETLNNDTQODKSTM 2146
Db 1277 RS-----NNNNFNINISRNLYDK-----KDLDLYENRNDSTYVELIKKLAET 1320
Qy 2147 DTILDLLE-KYND 2158
Db 1321 NCKENEISVKICD 1333

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RESULT 10
US-10-732-923-3351
; Sequence 3351, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3351
; LENGTH: 1985
; TYPE: PRT
; ORGANISM: Plasmodium yoelii yoelii
US-10-732-923-3351

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Query Match 3.4%; Score 414; DB 5; Length 1985;
Best Local Similarity 18.3%; Pred. No. 1,9e-12;
Matches 417; Conservative 318; Mismatches 778; Indels 764; Gaps 102;

Qy 121 LCNKFPMMNSNDSSKAGHDLAEVCMAYEGESIKTHYPKYDSKYP-GSDFPMTMLA 179
Db 39 LYNNVDTLNSLSXVNTNKLIEL-----QEYKXKRYREKDIPIHTYNDT 84
Qy 180 RSFADIGIIRGRDLYLANK--KKQNGKETEREKLKELKIFKLIHD-----NL 228
Db 85 RGSKN-NNQIKONNIYFNNAAILYNNANNNDINIKTYNNYNNINMINDGINSKNL 143
Qy 229 -KDKFAQGRYNDEDPNFKYLRBDWMTANRETVWGAAMTCSKELDSSYFATCNDTQGP 287
Db 144 PSNKGNNYISEK-----GDMN-EKELDHYSNFNFN-ND-----176

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QY 288 SOTNHKCKCDKGNAGKPKRAGDGVITVPTFYVPOYLWPEWABDFCKRKKKLE 347
 Db 177 -----NRKGSN-----ONDIIINKKYLE 196
 QY 348 NLEKCRGKDXDEYRCSRYNGYDCEOTISRKGVKMGCTDPCFAGSYENMIDNRK 407
 Db 197 SLMN--INKNNDDEKXINFNVNDIKNNY-----FDNFKYKNT 233
 QY 408 QPDKOKXTTKEISDGG--RKKRAVGTTTKEGY-----EKSPYEKLNDGYVDAFL 459
 Db 234 ENNEKXTKPRRSNSNVHTRKHDTGKISNYLYNADMOAKINYNEKNGMRAVEKYI 293
 QY 460 GLLNNEKACXOITDQKINPKEVNSGGVGGSGGSGTSGASG--TNDE-----NGK 508
 Db 294 KXKKNENHNNNNHNLTNNDLNGNANGTTEMGNSSEIKXVNNKNTDNNLNMMNNYEN 353
 QY 509 TFF--RSEYOCPCDPCGVHKG--NOMERKTKYKIMRSKLYKPING 552
 Db 354 TYQNRNE-----SNGKVEHDLGKLANPDLNIRKKGHLVFNKNOMENESTYTNKMDHIND 408
 QY 553 KMWLLKSLKVVKDMMLKQWKEFCLTQNSSDG-----SVGSVTTGASGNS 601
 Db 409 KXENY--NFSFINENKITKN-----LTNNDDALNPKNFKKMDVKSIVCVCQASQOM 460
 QY 602 EKKELYDE-----MKCYKNEVOKVNVGSEVBEDEDELKAGGLCILNPKKN 649
 Db 461 ARLOHIEESROMLETEKMLLKKKKEKNEFKVGMADKEIDKHSOIKEKELISINKN 520
 QY 650 KEVSEAKS-----QNNHADIOKTPHDFFYVVAHMLKDSIHWRTRGLKSCISDGTMKCR 704
 Db 521 NEIDEKEXVNSIKSKYDNOAKELD-----KMECILIEN--KCK 559
 QY 705 NGC--NKKCDCEKXVOKETEMPRIKDHFKTOGIEBGYYFTTLEILKQFKEPTE 761
 Db 560 SKLYEYDEKFGQFNKKIKIEIEBEKEIEBOEKKNI-----KKNMLENR 605
 QY 762 E-NTENSIDABEABELKLOKIL--LENNENLAVNAGTEOKTILMD--LLNHEILNAT 816
 Db 606 EIDEKMLNMKEKEMLEMKELSELEKKEKII--DCEYNNLONKEBELARNRNMLI 662
 QY 817 KCKDCPLPEEDKRSRSDPSPDIPRPEEKEDDENEDDE-----DEVADDE--E 866
 Db 663 K-----ENBLKR-----IDKYNELIDELNKKKEIENDKXKMLNIDODEIK 705
 QY 867 TAKETEGSATDTTSLDVCPIGVKVLTKDNESLQDACSLKYGNNSLGWRCTPSEBP 926
 Db 706 LLNETNN-----IKKENEK-----EINY-----MKE 726
 QY 927 TTSSPKNCAICVPRRRLIYKLYDMATKTESPOASGSEASSTGTTTPDSKALKA 986
 Db 727 EIKKIRIMINDVEKMKRLMEDI-----BNTKNILMEKEMENTYKKEIENDKMKMKN 782
 QY 987 FVESAIETPLMHRKEEKAVAOEGAGHGLPRVE--EGSPREYDEBKLEKGIPOGFLR 1045
 Db 783 IEDE-----KEKYTYLEKFNENLEKSELOKKYDDENNRLQAEI----- 824
 QY 1046 QMFYTLGDRILFSGSNDTTSVSKDTPSSSNDNI--KNIVLASGSTEOREKXK 1102
 Db 825 -----NNEKKKINK-----RDNLEKQKVV-----EDEFRNKCEKYE 857
 QY 1103 EIKNFRKSTERSANLVSHPOTWENNGKTYHGMVCALTSKDLAAGVEKPKKIE-- 1161
 Db 858 E-----DIRKKNMLEE--ENMKY-----RIMEQOELBNY 888
 QY 1162 PENLDEANKKPKPOYOYVTVKLDENSGTSPRTTQOASSDNTPTTLTHFKRPTYFRM 1221
 Db 889 KKNVVLDBEEDKQKLYVOEKINL--EKENLVEKQIDIELKN-----FKN 933
 QY 1222 FEEWGESFCREKRLKQIKYDCKVNGDVGRCSGDGEACDSISTHDYSTVPSFNCPCG 1281
 Db 934 FKEKENENDIKIRIINLSOOKEDLNKEKENIEK-----EKDLBKIKYD----- 976

QY 1282 KHCSYRKWIERKKEIEPHKQSNAYGOOKTDATRNNGN--TEDEKCEKTLJETPPAKFLE 1339
 Db 977 --LDAREEGLANNDIKQWEXSRKRLFTBOLEKIKKXKBEILANDREL--KTKEN--DLIEKGT 1031
 QY 1340 RLKNGPCKTNKEYG--DDIDPEKDSKTFQHTLEYGCPCKFKTNQNGNGVSLANGCDG 1398
 Db 1032 EIKKKNELNKKKKEKSLDDELKS-----YSSKQ-----DR 1064
 QY 1399 DKSIDAK--ELAKXRSSTVDVWREVSNDNTNTPGDDLDKACOHANI--FKGIRKDVWKG 1455
 Db 1065 EKKJKEKTELOKVDOLV-----DKNSLKEKEIOFOMIEK----- 1102
 QY 1456 YVCGVDICEQTNINERTDGEYIQRALFKRWENFLEDYKINDKISHCIKKGSGKCI 1515
 Db 1103 -----EKELDEQT--VIOI-----DRNSL-----BAKQPL 1128
 QY 1516 NGCEKNSKLEKWIJEKIAEMENIKKRPNDYENKDPDYVKSILELIPKIAVANDOD 1575
 Db 1129 LIKEHEKOTE-YIOEOL-----KLHEOLKXND-----KSLKE-----KE 1163
 QY 1576 NVIKL-----CVFENSKCTLISNTQNNKENDAIQMLKXLGVAKXKCPKPSGEXOD 1629
 Db 1164 NEINLNLKLODCRSKNGKAIY--SLKXVNNRKLNNLSRISVSKXRVKAKAIGKXPD 1220
 QY 1630 CKEPPPLPEEDQNPENTLEPPKFCPTTQPPREKGEETGKNE--EKODEKSESEBP 1687
 Db 1221 IIR--RTRKRSINYNTNLE--INNSIOYISVINDNRKKNRFLKNGKNNLELSNEN 1273
 QY 1688 AKESGPAEAPPAESETETNPPEPPGTGPAAPSTPAPTPTPTPPLRPOADEPPD 1747
 Db 1274 FMOEG--NNMNFKY--NDTYD 1293
 QY 1748 STILOTTIPFGVALALGSIAPFLPKKTKKASVGNLFOILOIPKSDY-----DIPTLKS 1800
 Db 1294 NSMVD-----KNENIISNNSKNI--IDYGNVNNBEPEREN 1329
 QY 1801 SNRYIPYSDRYKGYTYMEGSDDEDKXAFMSPTTDTVTSSSEYEELINDIYVPSGPX 1860
 Db 1330 RNQIISNENDIYENK--NNDKRNKGY--PPRPR 1360
 QY 1861 YKTLIEVLLPESGNNTTASGKNTPSDPTENDIIONDIPSSKITDNEWOLKKEFISN--- 1916
 Db 1361 AN-----LEKOSYVNNNGKSERNDENDLYN-----DNTTYKKEKEDYDNMY 1405
 QY 1917 ---MLQNPONVNPVDYSGN--SSTNTYITTSKHNVDN--NTNTYMSDNM----- 1961
 Db 1406 GDHNNYNNNNHNTKXGNYENNNGNGYNSYNINMMNTNLIKMGSLDNDITKXNG 1465
 QY 1962 -----EENILPSIHGNI-----YSGEYSYVNMV 1988
 Db 1466 LRLNFOEKDQBNNMMLGSLAVNNLIESDIIIDTSNHYHFDNHNDDKYGEMSNRINICI 1525
 QY 1989 NSMNDIPINRDNVYSGIDLINDLSGGKPIDIYDEVLKRKENELFGTEBTKRISTONVA 2048
 Db 1526 NKNINFINDVNNINNNINSINSLKYKXNS--NVE-----ENDSFVEHNNKNNKXSC 1578
 QY 2049 KTTMSDPIHNOLELPHKMLDHRDMCEKXKXKEDILNKLXK--ENKKNINNSGKTIVSD 2106
 Db 1579 QNNNENGMSN-----KNPEKESLNLDSLAVQNMOSVNOISLMQSS 1621
 QY 2107 NKPSHN--HYLNTDVSIGIDM--DNPKTGELITNMDTNDOKSMTDPTLIDLEKYND--PY 2161
 Db 1622 KKAANNYNNKLSNISKATNSLKDTKRRANNNDYVYDDNESPKKEDNFNEFLBELNDGKYN 1681
 QY 2162 YDPYE--DIIYHVD--VEKSMDDIYVDH--NNVTSNMADVTKHIEKNIVN 2211
 Db 1682 SNFIEKGDDDFYNNMEKSLNDKSNMGEY--DHKNRNNYVTSKMDRKHVHTLKNNTNS 1737

RESULT 11
 US-09-924-154-15
 ; Sequence 15, Application US/09924154
 ; Patent No. US20020127241A1

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; GENERAL INFORMATION:
; APPLICANT: Narum, David L.
; APPLICANT: Sim. Kim L.
; TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use
; FILE REFERENCE: 05213-0465 43170-262105
; CURRENT APPLICATION NUMBER: US/09/924,154
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/722,525
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent version 3.1
; SEQ ID NO 15
; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Mammalian
US-09-924-154-15

Query Match      3.3%; Score 396; DB 3; Length 1086;
Beet Local Similarity 19.8%; Pred. No. 7,7e-12;
Matches 267; Conservative 150; Mismatches 357; Indels 576; Gaps 65;

QY      85 KONDVRSVAGAGYDNKKK--CSNGM-----TCAPRRHLGNKNF-----PMMN-----130
DB      25 KKKFIDTYSLYE--CGKKIKEMKMTCTDNOFKSNMLCAPIRIQLCIVIIIFSENEEYI 83
QY      131 -SNS--SKAKHDLAECMAKYEGE-SIKTHYPRKDYSGDFPMCTMLARSPADIG 186
DB      84 YKNDINNKKFENIL-----KAVKLESNLLVQKHNNENSK-----LCDDIRMSFLDYG 132
QY      167 DIIRGRDLYLGNKKKKKQNGKETEREKLQKLEIKFKTHDNLDKDEAKRNGDE-----241
DB      133 DIIRGRDLYLGNK-----TDYIKQPFKIFNN-----EYNNNLINDEL 170
QY      242 ----DPMNYKLRBDMWTANRETWGANM--CSKELDNSSYFRATCNDTGGPSQTHNK 293
DB      171 NNELNDEKNIKLRKEMWEXKEDIWEMTKENHDFIECKKFA-----214
QY      294 CRCDKGNAGNAGKPRAGDGVITVPTYPDYVQYLWFEEMADFCRKKKKLEMLEKQC 353
DB      215 ----KDE-----PQIVRMIEBMSKQPLDEKNVWLFIL-----242
QY      354 RQKDKSDEYRYCSRNGYDCEOTISRKGVKMGKGTDCFPAGCSYBNMIDNQRKOPDKOK 413
DB      243 ----RMTYN--ENMIIHNN-----CKQYNKWYQNNKKEM--271
QY      414 KYTKETISDGGKRRKAVGGTTTYEGEKSFEYK-----LKNDSYETVAFGLNN 464
DB      272 ----TFLSNEFNKIFPERNVQIHSNIFKYEKENNVDIIFGTLNY 312
QY      465 E--KACK--DITDGGKINFKEVSGGAVVGGSGGSGAGSTDNENKGFYRSEYQPC 519
DB      313 EYNNCKEKEPBLVSAKYLKAPNA-----KSPRIYKSK-----346
QY      520 PDGVOHKGQNMERTKYVKKM--RW-----SKLYEP--ING--KMWLLSKLVKVD- 566
DB      347 ----EHEESYVFGCGTKISKYKMKKNVCYNNKVTPEBVCPPRRQQLCLGYIFLIRDG 401
QY      567 ----MMLKXKNMK-----EFCLONSDGSVGVV-----TTG 595
DB      402 NEEGLKDHINKANYEAMHLKEKYENAGGDKICNALISYADIGDIVRGLDVRDINTNK 461
QY      596 AS-----CGNSEKE--LYDEM-----KCYGHNEVQKV- 621
DB      462 LBEKPOKIMGGSNSKKNNDNNERNKMKWKKORNLWSSMVGHIPKGTKCKKHNNNEKIP 521
QY      622 ----NVOGE--VEEDDELKAGAGCLPLNPKKNKEVSEAKSQQNHADIOKTFHDFPY 673
DB      522 QFLRWLKEGDEFCSEMGTEVKQLKIKC-----ENKNCSE-----556
QY      674 YVVAHMLKOSIMHRTKRLKSLSDGKTMCRNGCNCKCFCFEKMYQKTEKPIKDHRK 733
DB      557 ----KCKKACSS-----YEMIKERNEY-----577

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QY      734 TQEGIPGGYFTTLEILIKLQFLKEDTEENTENSLDABEAEHLKHLKILKLENNLAV 793
DB      578 ----NLOSKKFFSDK-----KLNKNML--596
QY      794 VNACTEQKTLM-----DKLNLHMLDAP-----KCKDC-----PL 823
DB      597 YNKFEDKAYLRSSKQCSNIEFNDEFTFPNNKYKACMVCENPSSKALKPITTNVPI 656
QY      824 PEEDKSR-----GRSADSPDIFIRPREKEDENE-----854
DB      657 ESKKSLSLTDSKNTPNSSGGGNGYGDRIISRDDVHHDGPREVSGEKEVPKIDAAV 716
QY      855 --DDDEBEVRDDEETAKETEGSATDTTSLDV-----CPVGVLYTKDNESLQDAGSLK 907
DB      717 KTENEFTSNRNDIE--GKEKSKGDHSSPVHSKDIKNEBPORVAVSNLPKIEKMSSDSIP 775
QY      908 YCGNNSRLQWRCVYPSGEPITSS-----DKNGAICVPPRRRLYIKI 950
DB      776 ITHIEAKGQSSNSDNDPAVAVSGRESKDVNLHPSRIKENEBGVYIKTDESSKGIISKI 835
QY      951 -VDWATKTESPQASGEASSTSGSTTPPDSKEALLKAFVESAAIETPFLMHRYYEKKAV 1009
DB      836 PSDQNNHSDLSQANEDSNQNKETINPSTKMLKEI-----HYK-----876
QY      1010 AOBGAGHGL-----PRVEGSPDYDP-----DKLKEG-KIPDGLRQMFYTLGD 1053
DB      877 TSDSDDHGSKIKSEIEPEKELTEESPPLDKTESAAGDKHESVYSADIFQSEIHN--D 934
QY      1054 YRDILFSGS--NDTTSVKDTPSSNDNLKNIVVLASGSTQEBRKNMKYKIKFRKCS 1111
DB      935 NRDRIVSESVVQDSSGSSMSTESIRTDN-----KDFK--T 967
QY      1112 TERASPLVNSHPQTMWENNNGYIWHGVNCAVLTSKDKIAKGVKKPQKLENNIMDEANK 1171
DB      968 SEDLAPSLNGH-----EKIG-----SSADD--RGEDEDIIXDKSENF--ENNK 1007
QY      1172 KRPKPQYQVNVKLDENSGTSPRTTQIAS 1201
DB      1008 S-----SHSDIKQSDNKGSTDYESLTRES 1031

RESULT 12
US-10-732-923-15035
; Sequence 15035, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 15035
; LENGTH: 6761
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-732-923-15035

Query Match      3.3%; Score 395.5; DB 5; Length 6761;
Beet Local Similarity 18.0%; Pred. No. 8,2e-11;
Matches 489; Conservative 380; Mismatches 907; Indels 935; Gaps 123;

QY      36 NYVSELKSLSLASLIGETAFVVMQRESKYTELIBANSKKNPKCKQKQKGVDRFSVK 95
DB      162 NFLDGHKKSIFLKS--RNNVNTFQSDINSSKTSFSCSLKAM-----NYANDINKYS--213
QY      96 EQAGYDNKKMKCSNGMTCAPFRRLHLCNKN-----FPN-----NNSNDSYAKHDL 141
DB      214 ----NYNMMKINL-----HKLMLKKNKNDKJLFTNTSDKKNYVCALNGDHIIINCKDS 264
QY      142 IAEV-----CMAAKYEGESIKTHYK--YDSKYTPSGDFPMCTMLARSPADIGDIIRGRDL 194

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Db      265  FSDTIVSYGCRKRWKCKK-KNIYNNMLFYDESI--NDVYYKNLEKTEFTSNSSKIY---EL 318
Qy      195  YLGNKKQKQ-----NGKETREKLE-----214
Db      319  FENNYKFKKILNIECSGNKYKGLRTNHPPYANFNFTIRRLQ'SNVLGHFMISKCNFN 378
Qy      215  -----OKLKEIFKXIHNDLKDEAQRVNGDEDPNFYKLRJEDMMTANRETVGAMTCSKE 269
Db      379  RITCYRKTIKCVNKKRKNKRNVI-----NMYYKEN--VDSIKGTGNNNGVH 426
Qy      270  LDNSYFPAATCNDTQGSQ'SOTNKKCRCDKGNAGKPRKAGDVTYIVETYPDYVPOYLK 329
Db      427  HNNS---RRLNNTSKNNISNNNNMMLKXGKQKQYKGS-----FDQMIQ-- 468
Qy      330  WFEBAADPCRK-----KKKLENLEKQCGKQKSDERYCS---RNGYDC----- 372
Db      469  --EDTTLDOAKKESIKTVSKNERKNNMNGHSHDNVYSKLNKMSNKRNNKNCNPSNDC 526
Qy      373  -EQTISRKGKVMGKGTDCFPAGCSYENWIDNOKRQPKOKKTYKKEISDGGGRKKRBAVG 431
Db      527  NEDVIYK-----ICTTBEVNDDEKKKQJSRHKGFVCE-----RKKGYI- 565
Qy      432  GTTKYEGEKSFYERKLNQDGYTVDAFLGLNNERAKCDITDGKINFK--EVNSGGGV 489
Db      566  -----LONNNKCKKXNDNIIINNNDVNNCGDI 595
Qy      490  GGGSGGTGASGTNDENKGTFRSEYCOCPDPCGVQHGKGNOMERTKY--KKRWSKL 546
Db      596  NDHNRKDYDTTEBQNCPRKILSNFIKCEDEKLEFKIYNDWFLRIGIKVTNKRKKYFLI 655
Qy      547  YKPIGKM--VLLKSLKY-----VKDMMILKKMKWEKCLQNSSDGSVGSVVTG 595
Db      656  YKIVDSFPRILITFTEKLEKNIILQVMAQVITLDCKNVK-----IYSDP 700
Qy      596  ASGNSSEKELYDEWKCYKNEVQKYNVQGEVE--EDDELKAGAGLCILPNKRNKE--VS 653
Db      701  IYIRNNNTLYAKFKLITSKMYKKYKNNSEVNFDDBECK-----KEMKDNIS 749
Qy      654  EAKSONNADIOKTHDFPYVVAHMLKDSIHWRTRKLSGISDGKTMKCRNGCKKDC 713
Db      750  ESSKSNNGEKKMLH-----765
Qy      714  FEKWKQKETEKPIKDHFKTOEGIPEGYFTTLELILKLOFLKEDTEBNTENSIDABEA 773
Db      766  ---VEKSEBHDMTSDSNKEDTKIEG-----RKKSNNVNIIDVDVG 803
Qy      774  EELKLOKILKLENENILAVNAGTEOKTLMDKLNLHEND--ATRKCDPLPEEDKSRG 831
Db      804  EEEENVN-----NNDNN-----NDNNNDNNSDNNNDGSDNTECSKINSKYKG 851
Qy      832  RSADSPDIFLRPEKEDEDEDDEVRDEBETAKETTGSAITDTTSLDVCPIVGK 891
Db      852  K-----EKDOYKENTDD-----KNLSDSNSNNSKKKFKV---LNK 883
Qy      832  VLTKNESLQ--DACSLLKYGNNSLRGMRCVTPSGEPTTSSDPKN--GALCVPRRRRLYI- 947
Db      884  AIKONDKKKKYKKNKIBGNSNNMMLLVNSNSSSTSTSNSSSKSSNCRNKNQOISIC 943
Qy      948  -----KIVDMATKTESPOASGEASSTSGST-----TPPSKEALLKA 986
Db      944  SKMDEKNSBQKKKNKKKKNT-----CNEGSKKDSITLNCVKKYKKSJTDKQKQSKI 997
Qy      987  FVESAIETFLMHRYYKEEKAQVAGAGHLPRVEBGSPEYDPDKLEKGI PDGFL-- 1044
Db      998  NIKN-----EKKKKINNS-----KINKGRKGINKDK--GKGDNNNYVC 1034
Qy      1045  -----RQMFYTLGDYRDL--FGSGNDTTSVSKDTPSS--NDNKNIVLLASGSTEQR 1095
Db      1035  LIYDEKKEFYENFKKFDIINIVIKGSDSDESTRFYVDJNNNNNNNNK-- 1080
Qy      1096  EKNKRYKEIK-----NFRKCSSTERSAPNLVSHPOJTWENNKGXYIW 1135

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Db      1081  KMKLFFKVEKSLYLENIDIDTDEILFRPRPKRFNCIIEESPENYDINE--GEDGNFYVF 1138
Qy      1136  HGMVALNSKOKIAKGVKPKQKIENPENLWDEA-----NKK----- 1172
Db      1139  KNKLAKIKKKVTTIKNETDSSDMYIE---LKDBEGFRTIGRVSEFLKQKKAQOYKV 1194
Qy      1173  -----PKPPOY---QYTNVLDENSGTSBRTTOQASDNTPTTLTHPYK--RPTYFR 1220
Db      1195  GIKEYSPKYOQFHLHLENKLYQTSOLS---KGNNNNNNNNNKENGOFVCGHNSYSR 1250
Qy      1221  WFEWGESFCBERK-----KRLKOIKYDCYEN--GDVGRSGDGEAC---DSISTHYS 1270
Db      1251  -----ACSKSINSIYINKYKVELNEKITTNIIDNNNNNINSICIKYKNLSENENL 1302
Qy      1271  TVPSNFCGCGHCSYRWKIERKKIEPHKSNAYGOQKTDATRNGNTPDREFCKTJET 1330
Db      1303  CADKYLCOG-----NY-NMLEN--DVDEMANNDONOK---KENDLVF---SDYKG 1343
Qy      1331  WPDAAKFLERLKNGPCTKNKEYGDDI---DFEKD-----SKTFOHTEYCGPCPK--F 1378
Db      1344  WSPYFVNIKILN-----NYKEFERDILEKCDKKEMTDHYNNTLNKNEIGSISGKRLIF 1399
Qy      1379  KTNCGNGCGVSGLNGCDGKSIDAKELIARSTTDVNRV-----SDNTNTFBCD 1432
Db      1400  MKGHDHYSCLS--SAIYDMCSAEKKEIDE--NNCIDIYNGIKCFCEKXYHANCLJED 1455
Qy      1433  DLKQACQANI-FKGIARDVWKCGVYCGVDICEQININERT--DGKEYIQIRALFKRWYEN 1490
Db      1456  VLTTFPKDNLIMKEYKFIYKNSLKKEKRYFNNGKRRKTKNGK-----KQNTIH 1507
Qy      1491  FLEDEKINDKI-----SHCIKKGEKSGKJNGCEKNSKLEKWIIEKKAEMENIKRPN 1544
Db      1508  KLEBDK--NSHVSTASNSHSEIYVSSSESARKGNEKNTATCKRTSCSALYKVKKQKN 1565
Qy      1545  DOYENKQDPYV--VKS--LLEBLPKIAVNDOD---NVIKLCVFENSAGCTLIANT- 1595
Db      1566  KNGENKNGENNGDIDKNDIDKNDIDKNDIDRNDIDKNDENE-----ENTYCKNESNNI 1619
Qy      1596  QNNKENDAI--DCHMLKLGVAKNOPGK-----PSGE-----KQSDCKE----- 1632
Db      1620  DNNSSNDSLSLDVDNNKNGKSKNKKYRCINJIYPSVHSDITYKKFKCDQCRICYCE 1679
Qy      1633  -----P-----PPLPD-----BE 1640
Db      1680  SIYDKQTPNVAANYICAKGNMAHAGSCCFPNVPIYLFPMKKDCDLKCNKNYSNLGYI 1739
Qy      1641  DONPEENTL-----BPPKCPPTTOPPEEKGETCGNKEKDEK----- 1681
Db      1740  NYNWEHLHLDCCINCYKEKKNFC-----IMCNEKYDEDSKKVQCDVCVF 1787
Qy      1682  ---ESEBPAKEE--SGPAABEAPPAE---SEETE-----TNFEPFGT 1718
Db      1788  WIHLSCDNKESRNJETLSNKNIDYKCPYCSIGTFHDKIERILYLLFLLDKYNF----- 1841
Qy      1719  GPAAPESTPAP-----PTPDTPEPLRPOADEPSTLLOTTIPFGVALAGSIAF 1768
Db      1842  -----THVFINISYIRIYKIPANLYIMKKKIIEKKYDITLIDLYPMLIINHAKVH 1895
Qy      1769  L-----FLKKKTASVGNLFOIIOIPKSDYDIPTLKSSNRYIPIYVSADRYGK--- 1815
Db      1896  MPNTPIYGNACIPEKKGVIILKNMFM-----TNEYLNKICIDCEVNEYKNEINN 1944
Qy      1816  -----TYIYEGSDEDEKIAFMSD-----TTDVTSESSEYE 1846
Db      1945  LDSFOIGHNNNNNNNNNNNNNNNNKMEGVNNE--SVIEMDGNCKNLKYNKEGTMTVCNMOSI 2003
Qy      1847  ELDINDIYVPGSPKYK-----TLIEVULBPSGNNTTASGKNTESPTRNDIQNGI 1896
Db      2004  NKNLNDNNNNNNNNNNKMEFVPGQNNIKLANEYIINKEGNIISNDNNMYDYNNVQNGIM 2063
Qy      1897  PSSKTTDENQOLKEFISNMLQNOPDVPND--YTSGNSSTNTNITTSRHHVNDNNTNT 1954
Db      2064  KMYTNTINDVNS-----SNVPMESYVKNKENFTINNSI-----YNINENNTY 2104

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QY 1955 TMSRDNMEENLLPSIHGNYSGE-----EYSYVNVNVN----- 1989
DB 2105 DL---NCKKXIJFQKXNYLSAQONEGDIANNYNGWYQKININISNPYNNNNNNNNMAYEG 2161
QY 1990 -----SANDPIPNRNNNYSGIDLINDLSGKFPIDIDEVLKREKENVLFGENTKR 2041
DB 2162 EKYILNNDNMNINSISKNDINNCCNMIANYRKRKLQYKXKDIQYELFDFKDNDF 2221
QY 2042 TSTONVAKTNSDPIHNOLE-----LFHKMLDRHRD----- 2072
DB 2222 FINKRKFSGCSNDHNLIDYIILYKLANGKIYFTFPDKHDFPVCKILKXHLKNNRR 2281
QY 2073 -----MCEKWKX-----KEDIL-----NKLAEWNKENINIS----- 2099
DB 2282 GCGNHIMCPKIRNNQNLKEDYVQCDEBKIQNDNGCDEYDNNNNNNNNIGSSSISIN 2341
QY 2100 ----GRTY---SDKKPSHN-----VLTDSVIOIDMDNPKTKNETMTDNTQKSTMDT 2148
DB 2342 KIHMDTYNNSINDSLRNNNSCVFINSNI-FMIDVINEKVINNIYKETRILISPIIN 2400
QY 2149 ILDDLEKXNDPYDYDFEDDIYHDVYEKSSM-----DDIYVDHNNVTSNMMDVPTK-MH 2203
DB 2401 VLKFLKCIQIYVFYDNNTECTEKEKNVSSNLCNNFEEKYVINSIDHNNMSGEKKKS 2460
QY 2204 IE--NNIYVNNK 2212
DB 2461 VEIIMSVDNK 2471

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RESULT 13
US-10-087-013-11
; Sequence 11, Application US/10087013
; Publication No. US20040062769A1
; GENERAL INFORMATION:
; APPLICANT: Arthur Scherf
; APPLICANT: Louis H. Miller
; APPLICANT: Benoit Gamaun
; APPLICANT: Dror I. Baruch
; APPLICANT: Pierre Buffet
; APPLICANT: Christine Scheidig
; APPLICANT: Uurg Oyein
; APPLICANT: Bruno Pouveille
; APPLICANT: No. US20040062769A1utaka Fujii
; APPLICANT: Joseph Smith
; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; FILE REFERENCE: NIH176.001C1
; CURRENT APPLICATION NUMBER: US/10/087,013
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/24195
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,023
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 11
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-087-013-11

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Query Match 3.2%; Score 386; DB 4; Length 308;
Best Local Similarity 24.5%; Pred. No. 5,1e-12;
Matches 104; Conservative 59; Mismatches 123; Indels 138; Gaps 14;
QY 917 WRCVTSGEPTSSDKNGAICVPRRRRIYIKIIVMAWTESPOASGEASTSGSTTP 976
DB 20 WDC-----KKNIDNSHSGA-CMPFRQKLCVRL-----TQGEIIRK 55
QY 977 PDSKALLAFVSAALIEFFFLMHRYKEKKAVAGAGHGLPRVEGSPEDPDKLKE 1036

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DB 56 P---EDILTKFINCAAKETHFAHKKYKD-----NVNAENELKS 91
QY 1037 GKIDGFLRQMFYTLGDYRDLFSGSDTTSVSQDTPSSNDIKNIIVLASGTE-QER 1095
DB 92 GKIDGFRKQWYVYFGDFRDIFFGTDISCRYYIKDITQTKSLGDATTEKGTHTIDN 151
QY 1096 EKXNKYEIKNFRCSATERAPNIVSHPOVMENNGKXIMHGWCAITSKDKIAKGYEKK 1155
DB 152 KKL-----QEWYTHGPKINEGMLCALT----- 174
QY 1156 POKIENPENLWDEANKPKPPQYQYTWVKLDENSGTSPRTTQTOASSDNTPTTLTHFVKR 1215
DB 175 -----NGLSBEKKNIIDQYSYNKLN-----NMEKDDCCLEKFAK 210
QY 1216 PTYFRWFEWGESFCRERKRLKQIKYDCXYENGDVGRCSGDGACDISITHYSTVPSF 1275
DB 211 PQLRMVYEWEDCECRERK-----KLEDKYE--DVCIKADYEGCKNNKSN----- 255
QY 1276 NCPGCGHCSYKRWIERKIEFHKQSNAYQOQKTADTRNNGNTFDEKFCETLETWPDAA 1335
DB 256 ---SCVVCXEYENYITGKTKQYESQEGKEFTEKQ-KKEPYNYSK-----DAS 302
QY 1336 KELE 1339
DB 303 EYLK 306

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RESULT 14
US-10-153-273-18
; Sequence 18, Application US/10153273
; Publication No. US20020169305A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,273
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FMDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

MOLECULE TYPE: peptide
HYPOTHEITICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-153-273-18

Query Match 3.1%; Score 379.5; DB 4; Length 362;
Best Local Similarity 31.3%; Pred. No. 1.4e-11;
Matches 93; Conservative 14; Mismatches 149; Indels 41; Gaps 5;

QY 113 CAPFRLHLCKNFMNNSNDSSKAKHDLAEVMAAKYEGESIKTHYPKYDSKYPSDF 172
DB 2 CAPFRLHLCDY---NLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 58
QY 173 PWCMLASFADIGDIIRGRDYLIG--NKKKQNGKETEREKLEOKLKEIFPKIHNDLKD 230
DB 59 QLCVLASFADIGDIVGKDLVLYGDNCKXXXXXXXXXXXXXXXXXXXXXXXXXXXX 118
QY 231 KEAQRYNGDEDPNFKLRBEDMTANRETVMGAMTCSKELDNSSYFRATCNDTGGPSQT 290
DB 119 XXXXXXXKGGD---FFQLRBEDMTSNRETVMKALCHAXXXXXXXXXXXC----- 164
QY 291 HNKCRCDKGANAKGPRAGDGVITVPTFYFDYFQYLRMEEMADEFCRKKKKLEMLE 350
DB 165 -----XXXXXXXXXXXXXXXXXXXXXXXXXVQYLRMEEMADEFCRKKKKLEMLE 214
QY 351 KCRGKDKSDEYRYSRNGYDCEQTI SRKGVRMKGCTDPCFAGSYENMIDNQRK 407
DB 215 KQ-----CXKXXXXXXXXXXXXXXXXXXXXCTNGSVMCRMETWIDNQRK 259

RESULT 15
US-09-924-154-17
Sequence 17, Application US/09924154
Patent No. US20020127241A1

GENERAL INFORMATION:
APPLICANT: Natum, David L.
APPLICANT: Sim, Kim L.
TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use
FILE REFERENCE: 05213-0465 43170-262105
CURRENT APPLICATION NUMBER: US/09/924,154
CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 60/223,525
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17

LENGTH: 1501

TYPE: PRT

ORGANISM: Mammalian

US-09-924-154-17

Query Match 3.1%; Score 376; DB 3; Length 1501;
Best Local Similarity 19.1%; Pred. No. 1.3e-10;
Matches 300; Conservative 195; Mismatches 477; Indels 596; Gaps 70;

QY 85 KGNVDRESVKEQAGYDNKKM-----KCSNGM-----TCAPFRLHLCKNKF 126
DB 414 KNNDCSFNAQTDVYSSDRFCLKEKFKPKCDKNSFETVHHKGVCSPRQFCIGNL 473
QY 127 PNMNSNDSSKAKHD--LAEVMAAKYEGESI-KTHYPKYDSKYPSDFPMTMLARSPA 183
DB 474 -NYLLNDDIYVNHNSQLIEIIMASKQBGKLMKKGHTILDNO-----NACKYINDSYV 526
QY 184 DIGDIIRGRDYLIGKK--KKON-----GKETEREKLEOKLKEIFPKIHNDLKD 232
DB 527 DTKDVLIGDNLNDNNSIKVQNNLILFERNFYKVGKMKLFTKKE----- 573
QY 233 AQKRYNGDEDPNFKLRBEDMTANRETVMGAMTCSKELDNSSYFRATCNDTGGPSQTIN 292
DB 574 -----LKNVWMLLNKMKVSWRCG--IDVDQRRKTCG----- 605

QY 293 KCRCDKDGANAGKPRKAGDGVITVPTFYFDYFQYLRMEEMADEFCRKKKKLEMLEKQ 352
DB 606 --RIDE-----LENNPQFRFMFSQWAFHFCHEKEWELKLANDK 641
QY 353 CRGDKSDEYRYSRNGYDCEQTI SRKGVRMKG-CTD--CFAGSYENMIDNQRKQF 409
DB 642 CTGNN-----GKSLCODKTCQNNCTMNTQYTYTRKILAY 674
QY 410 DKQKTYTEISDGGRRKRAVGTTKYGEYKSF-YEKLKNDGYTVDAFLGLANNEKAC 468
DB 675 EIQ-----SVKDKDKRLFSIADKN-----VTFP-LKENAKNC 707
QY 469 KDTGKINPFEVNSGGVVGSGGSGTSGASGTDENKGTFRSEYCCQPCDGVQHK 528
DB 708 SN-----IDFTKI----- 715
QY 529 GNQWERKTKVKKRMSKLYKPIINGKMLLLSKLVKDMILK-KNWKFCITONSSDGS 587
DB 716 --FDQDLKLFERCSG--DQYLVGNKEMLSIDNSBD-- 751
QY 588 VGSVYTTGASGNSKELDYEMKCYKNEVQKVVNGVEEDELGAGGLCLPMPK 647
DB 752 -----ATDISRNGE-EELY-----VNNSVSVASGNKEIKSKDE--KQPE 790
QY 648 KNKEVSEAKSONNHADIOKTFHDPFYVVAHMLKDSIMHRTKLSKISDGTMKCRNGC 707
DB 791 K-----EAKQNGITLVATD-----KDSR----- 810
QY 708 NKKCDCEFKKWKQKETEKPDKHEKTQEGIPGYFTTLBLILKLOFLKEDTEENTENS 767
DB 811 NKG-----KDATDKNSPENILKVOEHGTNG-----ETIKEPPLPRESS 850
QY 768 LDABEAEFLKLOKLENNENLAUNVAGTQKTLMKLNLHENDATCKDCCLPRED 827
DB 851 ETLQSOEOLFAEAKQKQKEB-----PKKQEEBPKKQKE 885
QY 828 KSRGSADSPDIFIPREEKEDDENEDDEVDYDDEBT-----AKETEGSAT 877
DB 886 EEOQRBOE-----QKQBOEBEEOQEOIODOSQGLDOSKGVASQONWISGG 937
QY 878 DTTSLDVP-IVGKVLTKDNESLDACSLKYGGNSHLGRVYPSGEPPTSDKNGAI 936
DB 938 QEOVKSSEPEVPQETTSNGSGQD-----KISSTEPENS----- 975
QY 937 CVPPRRRLYIKIYDWTATKTES--PQASGSBASSTGCTTPPSKALLAFVESAIE 994
DB 976 -----VDRATDSMNLDPEKVHNHNSDPNTTEPDAS----- 1008
QY 995 TFFLMHRYKEBKAV--AOEGAGHGLPRVEBSPEYD--PED-KLKEGKIPDGLRQMF 1048
DB 1009 -----LKDKKEVDKAKKELQSTVSRIBSNEQDVOSTPREDPTVVBKV----- 1052
QY 1049 YTLGDRDILFSGSNDTTSVSK-----DTPSSNDNLKNIVLASG--STEOBERKNK 1100
DB 1053 ---GDKXEMLSRPHATDSBSBSGLNPTDIIKTIDGVVKEGELIGGSATETSJNLEK 1109
QY 1101 YKEIKNFKSCSTERSAPVLVSHPQTMENNNGKIYHGVACALTSKDKI--AKVEYKPP 1156
DB 1110 PKDVEP--SHEISEP-----VLSGTYGEBEELLSKSIETKG 1145
QY 1157 Q--KIENPMLPANKKPPPOYQYTNVGLDENSGT-----SPRTQTOASD----- 1203
DB 1146 EIDPSNDEQEDATDVENSDNNNSLSN-SVDNOSVNLAREDPASLETVEVSEBEDSR 1204
QY 1204 ---NTPTTLTHFYRPTYFRWFEBWGBSPCRERKRLKQIKVDCKYEN--GDVGRCSGD 1257
DB 1205 IITTEVPSTT--VKRPDEK-SEEVGE-----KEAKEIKVEVVPRAIGEPNENSVS 1253
QY 1258 GBACDSISTHDYSTVPSFNCFCGCGHCSYKMI-ERKKIEFHKOSANVGOQKTDATANN 1316
DB 1254 VQSPNVEDVEKETLISEN--NGLNDHTHRGNISSEKDLIDILHLNRNAGSGTILDDSHRN 1310

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QY 1317 GNTFDEKFECKTLETPDPAKFLERLKNGPCCKTNKEYGDDIDFEKDSKTFQ-----HTE 1370
Db 1311 G-----EMTBSES--DVGEIQEHNFSTQKDEKDF--DQIASDREKEIQLINIGHEE 1361
QY 1371 YCGPCPKFTKNCQNGCGVGLNGNC--DGDKSIDAKEIAMRSSTTDVWVRSNDNTNT 1428
Db 1362 DEDVLKMDRTEDSMSD---GVNSHLYNNLSSSEKMEQYNNNRDASKDREILNRSNTNT 1417
QY 1429 FEGDDLKDACQOHANIFKGIKRDVWVKCGVVGVDICEQTININERTDGEYIQIRALFKRW 1488
Db 1418 CSNEHSLKYCOYMERKDL-----LETCSE----- 1442
QY 1489 ENPLEDYVKINDKISHCIKGGSGKINGCEKNSKLEKWIKKIAEWENIKKRFNDQYE 1548
Db 1443 -----DKRLHL-----C---CEISDYCLKFFNPKSIEYFDCTQKEFD--- 1477
QY 1549 NKDQPDYN 1556
Db 1478 ----PTYN 1481

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Search completed: December 29, 2005, 23:40:09
 Job time : 275.987 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 23:15:22 ; Search time 14.2054 Seconds
(without alignment)
1174.559 Million cell updates/sec

Title: US-09-508-967-1

Perfect score: 12100
Sequence: 1 MATGGSGGCTGDEDAKHVLD.....VNNKEIFEERYPIDIMNI 2228

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 57103 seqs, 748879 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:*
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB pep:*
2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB pep:*
3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB pep:*
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5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB pep:*
6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267	2.2	5024	US-10-793-626-2964	Sequence 2964, Ap
2	212	1.8	1448	US-10-485-517-212	Sequence 212, App
3	210.5	1.7	4384	US-10-821-234-1120	Sequence 1120, Ap
4	204.5	1.7	1279	US-10-793-626-3188	Sequence 3188, Ap
5	192.5	1.6	948	US-10-485-517-131	Sequence 131, App
6	191.5	1.6	1596	US-11-060-005-4	Sequence 4, Appl
7	174.5	1.4	1155	US-10-793-626-1780	Sequence 1780, Ap
8	170.5	1.4	1163	US-11-044-899-2	Sequence 2, Appl
9	170.5	1.4	1163	US-11-044-899-30	Sequence 30, Appl
10	166	1.4	964	US-11-089-551A-30	Sequence 11, Appl
11	164.5	1.4	2314	US-11-013-759-11	Sequence 11, Appl
12	164	1.4	454	US-11-089-551A-35	Sequence 35, Appl
13	163	1.3	895	US-10-485-517-129	Sequence 129, App
14	162.5	1.3	3803	US-10-995-561-773	Sequence 773, App
15	162.5	1.3	3960	US-10-995-561-771	Sequence 771, App
16	162.5	1.3	5335	US-10-995-561-777	Sequence 777, App
17	162.5	1.3	5415	US-10-995-561-779	Sequence 779, App
18	162.5	1.3	5464	US-10-995-561-775	Sequence 775, App
19	162.5	1.3	5935	US-10-995-561-776	Sequence 776, App
20	159	1.3	1116	US-10-485-517-238	Sequence 238, App
21	159	1.3	1117	US-10-485-517-206	Sequence 206, App
22	158.5	1.3	910	US-10-793-626-3108	Sequence 3108, Ap
23	158	1.3	703	US-10-467-657-7158	Sequence 7158, Ap
24	157	1.3	1178	US-11-044-899-29	Sequence 29, Appl
25	155.5	1.3	877	US-10-485-517-200	Sequence 200, Appl

26	155	1.3	1531	US-11-087-227-24	Sequence 24, Appl
27	154.5	1.3	793	US-11-060-914-2	Sequence 2, Appl
28	154	1.3	1531	US-11-186-284-211	Sequence 211, App
29	150.5	1.2	290	US-10-821-234-862	Sequence 862, App
30	150	1.2	1976	US-11-069-834-54	Sequence 54, Appl
31	149.5	1.2	1095	US-10-793-626-3154	Sequence 3154, Ap
32	147	1.2	1976	US-11-069-834-52	Sequence 52, Appl
33	147	1.2	2096	US-10-995-561-606	Sequence 606, Appl
34	147	1.2	2351	US-10-995-561-608	Sequence 608, App
35	144.5	1.2	780	US-11-089-551A-22	Sequence 22, Appl
36	144.5	1.2	1770	US-11-103-957-21	Sequence 21, Appl
37	143	1.2	2053	US-11-013-759-9	Sequence 9, Appl
38	142	1.2	750	US-11-089-551A-32	Sequence 32, Appl
39	141.5	1.2	1207	US-10-821-234-1109	Sequence 1109, Ap
40	141.5	1.2	1346	US-11-060-005-2	Sequence 2, Appl
41	141	1.2	695	US-10-363-924-2	Sequence 2, Appl
42	141	1.2	710	US-10-467-657-4292	Sequence 4292, Ap
43	141	1.2	715	US-10-793-626-570	Sequence 570, App
44	141	1.2	744	US-10-873-528-184	Sequence 184, App
45	140.5	1.2	645	US-10-485-517-244	Sequence 244, App

ALIGNMENTS

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RESULT 1
US-10-793-626-2964
; Sequence 2964, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUJ480US
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2964
; LENGTH: 5024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; NAME/KEY: MOD RES
; LOCATION: (5024)
; OTHER INFORMATION: variable amino acid
US-10-793-626-2964

Query Match
Best Local Similarity 17.5%; Pred. No. 1.6e-06;
Matches 452; Conservative 356; Mismatches 970; Indels 810; Gaps 116;

13 BDAGVLDFFGQKNDVHG-----EAGVYSELKGSLSLSILBETATVYSKQTESKY 67
1437 QDITNALNNIKX-AODNLHGAGKLOODKRTTNOAIGNLN-----HLNQPODRL 1485
68 TELIANKKRNCKKDGKNDVRSVEKQAGDYDKKKKCSNGMTCAFRRLHLNKNKPP 127
1466 QAINATSTSDVYAEKLEKALDE-AMKOLEQVNVQDDQISNS---SPFIN----- 1532
128 MNNSNDSSKAKIDLLAEVCMAYEGESI-KTHYPRKYSKYPGSDFPKMTMLARSPADIG 186
1533 --EDSDKQKTVNDK-----QAAK---EIIQNTSNFTLDKQ-----KIADTLQNIK 1573
187 DITRG--RDLYIGNKKKKQNGKETREKLEQKLEIKFIKHNTL-----KDKKAQKRY 237
1574 DAVNNHDDQKLAQSKODANNQNLHLDLTTEEQKKNHFPFLINNADTRDEVNQDLTAQKL 1633
238 NQDDEPNFYKLRJEDWMTANRETVMGAMTCSKELDSSYFRATCNDTGQSPSOTHNKCRCD 297

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Db 1634 NGD-----MSTLHKVINDKQ-IOHLSYINAD 1660
 QY 298 KOKGANACKP-KAGGDVTVPTFYDPYVQYLWPFEBEAMEDRCRKKKKLEJFKQCRGK 356
 Db 1661 NDKKONVYNATKEABDLHNHPTLDH-----KALQDLANKIDQAHNELNESRFX 1711
 QY 357 DKSDEYRCSRNGYDC-----EOTI-----SRKGVRMGKGTDCFPACGS 397
 Db 1712 QALDN-----ALNDIDSLNSLNVPOQVYKDNINHVTLESIAQELQAKALEND---AMKA 1764
 QY 398 YENMIDNQRKQDKQKTKKEISDGGGRKRAVGGTTKKEGKESFYE-KLKNQDGYTVD 456
 Db 1765 MEDSLMNQ-EQIRKSNVTNEDLQAOONAYNHAVDINNIIIGEDNATMPQIIKQATODIN 1823
 QY 457 AFLGLNNEKACKDITDGGK---INPKEVNSGGVVGSGGSGTSGASGNDENKGTFRYS 513
 Db 1824 TAINGLNGDQKQADAKTDAKQOITNF-----TGLTEPQKQ----- 1858
 QY 514 EYCOCPDCGVQHKGNQWERTKVKYKRMWSLYKPNKGAVLLKSLKVVXDMMLKKN 573
 Db 1859 -----ALENIINQOTSRANVAKQJSHAKF-----LNGKM-----BELKVAVAKASLVARQ 1902
 QY 574 WKEFCLTONSSDGSVGSVTTTGAAGNSSEKELYDEMKCYKINEVOXVVOGEVEDDE 633
 Db 1903 NSNYINEDVSEKEAVEQALAKQGBIINSENNPTISSTDI--NRITOEIN-----DAEON 1954
 QY 634 LKAGAGLCILPNPKKNKEVSEAKSON---NHADIOKTFHDFPYW---VAHMLKD--S 683
 Db 1955 LHGENKL-----ROAQETAKKEIQMLDGLNSAQITKLQDIGRTTTRKAVTQKLEBAKA 2008
 QY 684 IHMRTKRLKCSID-GKTMKCRNGCNKCD---CEPKVYKQKETEWEKPIKDHFKTQEGIP 739
 Db 2009 INQAOQQLKQSLADKQATLNSSVYINDESEKLAAYDNAVSQAEOJLNQND----- 2059
 QY 740 EGYFTTLEILKQPLKEDTEBENTENSIDABEABELKLOKLIKLENNINLAV---VNA 796
 Db 2060 -----FTMDI-----SNIQAITQKVIQAKDS--LHGANKYLAQOASNNIINOSTVL 2104
 QY 797 GTEOKTLMKLNH-----ELNDATKCKDCPLREEDKSRGSADESPDIF 841
 Db 2105 NDKQKQALNDLINHAOTKQOAVBIIAQANKLNNEKOTLKTLYVEBGSNNHQSK-----Y 2158
 QY 842 IPRPEKEKEDENEDDEVRDE-ETAKETTESATDTTTSIDVCPVIGVY-LTKDN-- 897
 Db 2159 I-----NBDPOVNIYNDISIOGRBEILNGTTDVLNNKKAIDAIQNIHLTNDLH 2208
 QY 898 -----ESLQDACS-LKY--GGNSRFLGRCVTPGSEPT--TSPDKNAILCVPRRRRL 945
 Db 2209 GPOKQKQAOQDATTNELNYLTNLNNSQROSEHDEINSPARTEVSNDLHAKALNEAMROL 2268
 QY 946 -----YIKKIVDAKTESPOAGSEASTSGSTTPDSKEALLKAFVESAAIETEF 997
 Db 2269 ENEVALENSVKLSDITNEDEAAQNEYSNALQAKOIIINGVPSSTIDAKTIEDALLIELON 2328
 QY 998 LHMRYKEKKAAVQABGAGHGLPRVE-----EGSPREYDEBDKLEKGI 1039
 Db 2329 ARESLHGEOK-LQEAQNQAIABIDNLQALNPGVLABKTLVNVQASTKEVQALQAKGE 2386
 QY 1040 PGDFLFQMFYTL-----GDYDILFSGS-----NDTTS 1067
 Db 2387 LNEAMKALTEINKEEQIKADSRVYNADSGLQANVNSALNYGSOIATTOPPELKNQVIN 2446
 QY 1068 VSKDPTSSSNDNLKNTVLLA-----SGSTBOERBK----- 1097
 Db 2447 RATQTTIKTABNNNGSKLAEAKSDGNGSTIEHLQSLQSOQKQHLINOQTKQOYVDI 2506
 QY 1098 -----MNKYKEIKN-----FRKCTERSAPN-----LWSPQOTW 1127
 Db 2507 VVNSKOLDSNMQLOQIVNNIDNTVVKQNSDFINEDSSQODAYNHAIOAKDLIRAH----- 2562
 QY 1128 ENNGKTIHMGVCAITSKDIKAGVEKKPOKIE--NPEINMBANKKPPPOQYQYVNVKL 1185

Db 2563 -----TIMDKNOIDAIENTKQALNDLHSGNKLSF-DKXEASROLONLN--- 2605
 QY 1186 DENGSPRTTQTOAASDNTPTTLTHFYKRPDYRFEWESEF--CERKKRLKOIKVD 1243
 Db 2606 -----SLTINGQOK--TILNHFSAFTR--SOVEKELIASAKOLNNMTALR-D 2647
 QY 1244 CKVENGVGRCSGGEACDSISTHDYFVFPFNCRCQKHCSSYRKMTERKKIEPHKQSN 1303
 Db 2648 SIADNNEI-----LOSSRY-----FN-----EDSEQON 2670
 QY 1304 AYGOOKDTATRNNGTNPDKFECKTLETWPAKFLERLKNQPCKTNKEYGDDIDFERXS 1363
 Db 2671 AYNOAVNKA-----KNIINDQPTPVMADEIGSLANEVKQTKMLDHDQ-KLANDK 2720
 QY 1364 KTFQHTXGCPKPFKTNQNGNCGVSGLNGNCDGSDAKETAKMRSSTTDVYMRVD 1423
 Db 2721 TDAQATL--NALVYLNQAGNGNLETQVQNSN--SRPEYQVYVOLANQNDAMKDKLD 2773
 QY 1424 NDTNTEBDDIKDACQAHNIFKGIKRVYKKGVCYGVUDICEQTNINERTD-GKXEYQIR 1482
 Db 2774 ALTG--NDALQOTSNYIN-----EDTSQOVNFEYTDGKNIVABOT 2813
 QY 1483 LFKRWVENFLDYNKINDKISHCIIKKGESKINCENKSKLEKMEIKLIAEMENIKR 1542
 Db 2814 NPNNSPNI--NTIADKIT-----BAKNDIHGVOKLEBAQOQSI--NTINQMTGLNQA 2862
 QY 1543 FNDQYENKQDPYVYKSLBELPIKRIAVNODQNYIKLQV--FENSGCTILISNTQNK 1599
 Db 2863 QKEQJ-NQEIQOTGRSEVHQVINKAQALNISMVTLRQSIITDEHEVKOTSNYINETVNO 2921
 QY 1600 E--NDALIDCMKLQGVKAKNCRKPSGSKQSDCKEPPPLPBEODNPBENTLEPPKFCPP 1657
 Db 2922 TAYNNAVDVRKOII-----NQSNTPTNPLVEBRATSN 2954
 QY 1658 TTQPEBEKGETCGNKKEKDEKKESEEPAKESGPAEAPAPYAESEETETNPEPBG 1717
 Db 2955 VKTSDALHGE--RELNDKNSKTRAVNHLNDLNAQOEALTHEBOA----- 3000
 QY 1718 TGPAAPSTPAPEPTDTPPLRPOADEPDSITLIQTTIPFGVALAGSIAFLFKKTKA 1777
 Db 3001 -----TIVSQVNNIYNKAKALND-----MKKULD 3025
 QY 1778 SVGNLFQLOLPKSYDIDPLKSSNRYIPYVSDRKKGTYIYMEBDSDEDKAFMSDPTD 1837
 Db 3026 IVAQODNYRQ-----SNNYI-----NEDSTPQNMVYDNTINHAQSIIDQVAN 3066
 QY 1838 VTSSESEYEB-----LD-----INDIYVPGSPYKTLI--- 1865
 Db 3067 PTMSHDEIENALINIKALINALDGEHKQOAKENANLINSINDLMAIORALINLVBA 3126
 QY 1866 ---EVLPEPSGNNTTASGKNTPSDTRNDIONDG-----IPSSKITDNEMNQ----- 1908
 Db 3127 QTRKAVABQL-QSAQALNDAMKHLRNSIONQSVROESKYINASDAKKEQYNHAYREVE 3184
 QY 1909 -----LKEFEISNMLQ--NQPNQVFN-----DYTSNASTNT--NITTSRHNV 1948
 Db 3185 NIINEOHPTLDEKIIKOLDVANOANDLNGVELLDADKQNAHOSIPTLMLHNAQOQNL 3244
 QY 1949 DNNTTNTMSR-----DNMEENIL-LPSIHQNLVSGE---EYSYN-- 1984
 Db 3245 NEKINNAVTRAVAAIIGQAKLIDAMENLESIDKQVQOSSNYINBDPVQETYNNA 3304
 QY 1985 -----VNMVNSMNDI--PINRDN-----NYSIGIDLINDLSGGKPIDI 2021
 Db 3305 VDHTEIILNQTNPTLSIEDIHAINEVNOAKQKRGKQKIQOTIDLADKEIS--KLDDL 3362
 QY 2022 IDEVLKRENELFGENTKYSTQVAVKATNSDPIHNOLELPH---KILDHRQMCXK 2077
 Db 3363 TSQOSSSISNOYI-TAKTRTEVAQAIERAKSINHAKMLANKIYKQADKVLDSRFINEQ 3421
 QY 2078 KXKE-----DILNKLEEMN--KENINSGK-----TYSN 2105
 Db 3422 PEKEAYQOALINHVDSIHHRQTPBMDPYVINSITHELETAQNNLNGDQKLAIAKQADANV 3481

Qy	2106	DNKSHHNVLTWD	DSIQIDMNP	KTKKNEIT	-NMDTNQ--	DKSTMDT	-----	ILDD	2155
Db	3482	INGIHLNVAORE	EWAMINTN	-TNATTREKVA	KDLDAQALDRA	-METLQO	VAHKNNI	LND	3539
Qy	2153	LEKNDP	PYYDYF	IEDDI	YHDV	VEKKSMD	IYVDHNV	TSNNMD	VP
Db	3540	SKYLNEDSKY	QOQYD	RVI	-ADAEQ	OLL	-----	NQTN	P
Qy	2212	KKEIFEER	2219						
Db	3588	EKILFGAE	3595						

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RESULT 2
US-10-485-517-212
: Sequence 212: Application US/10485517
: Publication No. US20050256299A1
: GENERAL INFORMATION:
: APPLICANT: Universal of Sheffield
: APPLICANT: Biosynexus Incorporated
: APPLICANT: Foster, Simon
: APPLICANT: Mond, James
: TITLE OF INVENTION: Antigenic Polypeptides
: FILE REFERENCE: P100629WO
: CURRENT APPLICATION NUMBER: US/10/485,517
: CURRENT FILING DATE: 2004-02-02
: PRIOR APPLICATION NUMBER: GB 0118825,9
: PRIOR FILING DATE: 2001-08-02
: PRIOR APPLICATION NUMBER: GB 0200349,9
: PRIOR FILING DATE: 2002-01-09
: NUMBER OF SEQ ID NOS: 424
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 212
: LENGTH: 1448
: TYPE: PRT
: ORGANISM: Staphylococcus aureus
US-10-485-517-212

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Query Match 1.8%; Score 212; DB 6; Length 1448;

Best Local Similarity 18.4%; Pred. No. 0.00032;
Matches 286; Conservative 188; Mismatches 601; Indels 478; Gaps 64

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QY 583 SSSDSVSGVATTVGASG--SEKELVDWMCYKHNQKVNQSEVEEDDELK 636
D 167 NSQNDVDQAKTTGENSIDQVTPYWKAKATAREIIPALINKLQE--IQATPDATDEKQA 224
QY 637 AGGLCILPKNPKKNEVSEAKSONNHADIQKTFHDFFYVVA-----HMLKDSI----- 684
D 225 ADAEANTENGRKANQAIIS--AATTNAQVDEBAKANAEAAINAVTPKVVKKOAAKEDIDLOAT 283
QY 685 -----HWRTKRLKSCIDGK---TMCRCNCKNKKCOCFEKNVQKETE 724
D 284 QTNVINNDQNAATBEKEAIIQOLAAVAVTDKANNITAAITDDGVDAKAGKNSISTOPA 343
QY 725 WKPIKDHKEKQEGIEGYFFTLLEILKLQFLKEDTEBTENSLAAE---AEELKHLQ 780
D 344 -TAVSNKND-----VDQATTONQAIIDNTTGAATBEKNAKADVLKAK--KAYQ 392
QY 781 KILKLENNNLAVVN-----AGTEQKTLMDKLNHLEINDBTKCKDPLPEEDSRORS 833
D 393 DILNAQTTNDVQIQDAVADIGITATPTTKIDVAKDEL--ATKN-----EQKLLIQT 445
QY 834 ADPSBDIPPEEKED-----DENEDDEDEVRDDEBTAKETTESGATDPTTSL 883
D 446 ADAT-----TEBEQANQGVDAQLOLQGNQNIENAGSIDVNTKADNAIQALDPIQAST 498
QY 884 DV-----CPIGVKV--LTKNESLQD-----ACSLKYGGNSRLGWRCVTPS 923
D 499 DVKTARAAELLTEMQNKITELINNETTNEEKNDIGFVRAAYEBGLNNI-----NAATTT 554
QY 924 GEPTTSSRKNGAICVPPRRRLIYIKIYDMATKTSPOASGSEASTSGSTTPPDSKEAL 983

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Db	555	GDVTTAAO-----TAVQVAVQGLLHNPVKKAGKBLDGAADK--KTQIBQTPNASSQOEI	607
Qy	984	LKAFVESAAITFFLMTHERYKEEKAAVAGGAGHGLPRVEEGSPETDEPDLKEGKI PGCF	1044
Db	608	-----NDAKGEVDTE--LNQAKTNDVDSSTNEYVNAVNAVEGAKTINA	647
Qy	1044	LROMFYTLIGDRDLIFSGSNDTTSVSKOTBSSNDNLKNIVLASSGTGEOREKNNKYKE	1104
Db	648	VK-----TFSEKKKALAKIEDAYAKNAKVEADNSN-----ASTSEILAER--QKLAE	693
Qy	1104	IKNFRKCTERSAPBLVSHPOTWMENNKGTYIMHGVCALTSEKDKIAKVEKEKKQKIENE	1163
Db	694	LK-----QTAQGN-----YNATSKDIEVQIH---NLDNIN	723
Qy	1164	NLMDEANKPKRPO--YQYTVNKLDEMSGTSPRTOQOASSDNFTTLTHFYKRPYTRW	1222
Db	724	DYTIPTGKESGATDLYAVADQKKNIS-----ADTNATOD-----	759
Qy	1222	FEEWGSESCRKKRLKOI-----KYDCXYENGGVGCSGDGEACDSISTHDYSTV	1277
Db	760	-----EKQQAIKQVQDNQVOTALESSINGGVNDGVNDALTOGKAALDAIIVADATVK	809
Qy	1273	PSFPCGGCGKCSSYRKWIERKKLIEFHQSNAYGQOKTDATRNNGTPTDK-----EFCX	1324
Db	810	PKAN-----QALVYVAEDPTKSSIDQSDQTLBEKTEALAMI KOITDQAKOGITDAVT	861
Qy	1327	TLETWPAKFLERLKNQPCKTNNKEYGGDDIDEPKDSKTFQHTHEYGCPKFKTNCQNGN	1388
Db	862	TAIEVKAQAQGLAEAFDN-----IQIDSTEKQAIIELE-----TALDOIE	901
Qy	1387	CGVSGLNGCNGDXSIDAKEIAKRSSITTDVVMVSDNDTTFEEDDLKDACQHANIRKG	1444
Db	902	AGV-----NVNADATTEKEAF-----TNALB--DILSKTBE-----	931
Qy	1447	IRKQVMKGYCVGVDICEQTNINE-----RTDGEYIQIRALFKRVENFLDYDNKINDI	1502
Db	932	-----DISQDTNAELATYKNSALBOLKQORINPEVKGALAEIRVAVAKQ	977
Qy	1503	SHCIKKGSGKJNCJENKSCLEKMI EKKIAEWB--NIKRFNDQYENKQOPDYNVXSI	1566
Db	978	LEIKNMDADAS-----AKELARTDLGRYPRFADKLD--KTQTNABEVAL	1022
Qy	1561	LEELIPKIAVY-----NDQDVYIKLCVENSGCTLIISNTQNNKENDALDMLKULG	1611
Db	1022	QNVITIPALAEIIVPONDPDANTNGI-----DNNDAFANSNANATPENTG-----OPN	1066
Qy	1613	VKAKNCEK-----PSGEKQSDC---KEPPLPLDEEDQNPSENTLEPPKFCPTQOPPEE	1666
Db	1070	VSETTANCKADASPTTPNNSDAATGETTATISATDANDKPOAN---NSSVDASTNSPTM	1122
Qy	1665	KCGETCGNKEKEKDEKKEESEEPAKESGPAAEBAPTAESBETETNPPEPBGTPAAP-	1722
Db	1127	DNDVT--SKPEVESNTNGTTDCKPTEJTDNATPASTTNNGSTTATINENAPGSPATAPT	1188
Qy	1724	PSPTAPPTPTPPPLRPQADEPFDSTILOTTIPGVALAGSIAFLFLKKKTKRASYGNL	1788
Db	1185	TASTEASAASADS-----KDNASVSDS-----	1203
Qy	1783	FOIIOIPRSDVDITLKSNNRYIPVSDRYKGYTYIWEGSDDEDKYAFMSJTTDVTSSE	1844
Db	1206	KONABVNNNS---AESOSTINDKVOFASENKAKA---EKDG-----SDSTQSNVE	1244
Qy	1843	SEYEBLDINDIYVGPSPKYKTLIEVVLPEPSGNNTTASGKTPSPDTRNDIONDGIPSSKIT	1903
Db	1250	STTEBLPESADITEP-----NVPSPNTSKQKE-----ESTTN	1275
Qy	1903	DNEKNOLKCEFTSNMLQNPNDVPR-----DYSGNSSTNTNTTTSRANVDN---	1955
Db	1280	QTDAGOLKSE--TWASNEADSKSPSKADTEVSNKPSSTASASEAKEMKSTVNSQOKDPTAT	1337
Qy	1951	-NTATTTM-----SRDMNEENLLLPSTHIDGNLVSGEYSYVNVNVNWSGN	1992
Db	1338	ADTNDTKQSGVSAANNKATQNDGANAASPATVSNSS---NSANQDMLANTN	1384


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Db      3662  TATPQSGDGTVEINLEARNVETPTVEPSPSIPTSGEQCEGRTSSSGSEKS----- 3712
Qy      1460  VDICQNTINE-----RTDGKEYIQIRALFKRWENFLEDYKINDKISHCIKSGSKC 1514
Db      3713  ---AAATYTSKDPKLRTPKRGISASTMTWK-----KEGPEIYDKIEAVWTSCQG--- 3761
Qy      1515  INGCNKSCKLEKWELEKIAEMENI-----KKRPNDQYENKQGDYVAVSKIL 1561
Db      3762  -----LENETITMISTANSOMGVPRHEKIDFQKDNFNAN--NNLDSSTIGTDNIM 3810
Qy      1562  BELI-----PKIAVNDODNVNVL-----CVENSKCTLLISNTQNNKENDAI 1605
Db      3811  SNIVLTHSAPCTTEKONPVAVSSGKTVLQGHCVBKQK--VLGGQQTKEILIGR 3867
Qy      1606  CMLKRLGVAKA-----CPKPSGSKQS-----DCKEPPPLPDEE 1640
Db      3868  -OKSLPLIKATSPPKTFPPNHSNTKASKMKSQSEKTKALTSSCVDVKSRIPVKN-- 3924
Qy      1641  DQNPENLBPFPPTTQPPPEKGGTCGKKEKDEKKESEBEPAKESGPAAEBPA 1700
Db      3925  --TPDNITIAVKACATOKOGPEKG-----KAKQLPSKLPVAKNS----- 3963
Qy      1701  PTASEEETETNPEPPPTGPAAPSTPAPTPTDTPPLPQADEPFDSTIIQTTPFGVA 1760
Db      3964  -TCVTTTTT-----ATTTTTTTTTTSCIVAKRSQ----- 3995
Qy      1761  LALGSIAFLFKKKTASVGNLFQILQIPKSDYDIPLKSNRYPIVYSDRYKGTIYIM 1820
Db      3996  -----LKEVCXHSI-----EYFKGIS-----GETLKLIV 4018
Qy      1821  EGDSDEDK--YAFMGDTDTVTSESESEYEELINDIYVQSPKKYL-----IEV 1867
Db      4019  DRLSEEEKKMOSELSDDEESTSRNTSLSTSRG-----GQPSVTYKSAADKTEAPLKS 4073
Qy      1868  VLEPFGNNTTASGKTPSD--TRNDIONDGIPSSKITDN--EAMOLKKEFIENMLONP 1922
Db      4074  KSEKSGSEKRSRRRGPOSPCERDIR-----MAIVADHLGLSWELAREL--NFSVBEI 4126
Qy      1923  NDV---PNDYTS-----GNSNTNTITT--TSRNVNDNNTNTMTSRDNMBE 1963
Db      4127  NQIRVENPNLSLSQSFMLKKWVTRDGKATDALTSLVTKINRIDIVT----- 4175
Qy      1964  NULLPSIHGMLYSEBYSY--NVMNVMNSMDIPIRDNVNYGIDILINDLSGKPIDY 2022
Db      4176  -----LLESPITDYGNISGTRSPAD-----ENNVEH-----DPVD-- 4205
Qy      2023  DEVLKRENELFGENTKRTSTONVAKTTNSDPIHNOLELPHKMLDR--HRDMCEKMKV 2079
Db      4206  -----GMQN--ETSSGNLESCAQARVYVGL-----LDRLDSFDQC----- 4240
Qy      2080  KEDILINKLEEMWKNENINNSGTYNSDNKPSHNHVLANTDVSIIQIDMDN--PTKNEIITNM 2137
Db      4241  RDSITSYLVKGEAGKEANGS-----HTEITPEAKTKSYFPSSQNDVGRQ 4284
Qy      2138  DTNQ 2141
Db      4285  STKE 4288

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3188
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3188

Query Match      1.7%; Score 204.5; DB 6; Length 1279;
Best Local Similarity 18.0%; Pred. No. 0.00069;
Matches 283; Conservative 242; Mismatches 547; Indels 503; Gaps 75;

Qy      756  LKEDTEENTENSLOAEAEELKHLOKILKENNNLAVVNAAGTEOKTLMIDLIN--HELN 813
Db      1  VKSEARQAVONKAN---EQINHTQNTPDATNEEKQALINVSABLAARVQAOINAEHTQ 56
Qy      814  DATCKDCPLPE-----EDKSRGSADSPDIFIPRPEK-----EDDENEDDD 857
Db      57  GVKTIKDIAITSLSRINAGVVEKESARNA-----IQGKATQQTQFINNNDNATDE 106
Qy      858  EDEVRDEETAKETTESATDTTSLDVCYVAVKYLTKDNESLDACSLKGTGNNSRIGM 917
Db      107  EKEVANMLVIA---TKQKSLDNINSL-----SSNNDVENA---KVAGIWEI--- 146
Qy      918  RCVTPSGEPTSSSDNGALCVPRRRRLYIKKIYDMATKTESPQASGSEASTSGSTTPP 977
Db      147  -----ANVLPAATAVSKAKKDDIDQKLAQOINQOTHTQATTT----- 182
Qy      978  DSKBALKAFVESALETFFLHRYKEEKAAVAGGAGGLPRVE--EGSPEDPEDKLKE 1036
Db      183  EKEKALIDLANQK-----NEAKTALQNEHSNNGVAAQAKSNQIHFI-----E 224
Qy      1037  KIPDPGLQMFYTLGDYRDLIFSGSNDTTSVSKDTPSSNDNLKNIVLASGTEQRE 1096
Db      225  LVMPDA-----HKSDAKQSIDNKYNEQSNWTINTTPD-----ATDESKQ 263
Qy      1097  K-AMKYKEIKNPKRCKSTERSAPNLVSHQPTWENNKGXIYHGMVCAIISKOKIAGVEKK 1155
Db      264  KALDLKLIAKD-----AGYNKVDQAT-----NOQVS---DAK 293
Qy      1156  FOKIENPENLWDEANKKPKPQOYQYTNVKLDENSGTSPTTOTOASDNTPTTLTHFYVR 1215
Db      294  TEALDTITNIQANNAKKS-----ARVELDSKPEDLKR--QINATPRATE----- 336
Qy      1216  PTFYRWFEEWGESFCRERKKRLKOIYKDCVYENGDVGRCSGDGEACDSISTHYSTVPSF 1275
Db      337  -----BEKQDAIQRLNGKR--DEVK--NLINQD--RDNVEVEQHKNIQIQLLEFI--- 380
Qy      1276  NCPGGGKAGCSSYRK--WIERKKIEPHKQSNAYGQOKTATANNGTPTDKEFKTLETMPD 1333
Db      381  -----HANPTKRSDALQELQTKFISQTEILINNKK--DATN-----EKKDE 418
Qy      1334  AAKFLERLKNPCKT---NKEYGDDIDDFEKDSTKTFQHTEXGCPKPKTNC-----QN 1384
Db      419  AKRLLEISKN---KTTTINQAOQTNOVDNAKDNQAMEIATII--PATIKTKDAKTAIDKK 474
Qy      1385  GNCGVSGLNGNCDG--DKSIDAKEI-----AKXRSSTTDVVMKVSNDNTTFEGDDLK 1435
Db      475  AEOQVTTIINGNNDATDEKAEARKLVEKAKIEAKSNITNSPTEREVNGAKTN----- 526
Qy      1436  DACOHANIFKGIKRDVWKCGYVCVDICEQTNINERTD-----GKEYIQIRALFKRWEN 1490
Db      527  -----GLEK-----INNQPSTQRTYNAKQOINDKAQOQLQINNTPDATTEE 569
Qy      1491  FLEDYRKINDKISHCIK---KGEBSKJINGEKNK---KCLEKWEIKKIAEMENIKRF 1543
Db      570  KOEATNRNAGLQALQIINNNAHSQBYNEBSKTSIATIKYQVPRVICKPRAINSLTQEA 629
Qy      1544  NDQY-----ENKQDPDYVYKSLLEELIPKIAVNDODNVYIKLCEVENSIGCTL- 1591
Db      630  NNQKTLIGNDGNATDEKAAKQVLVTOQLNBOIQKIH--ESTODNOV-----DNVGAQAIT 683

```


RESULT 6
 US-11-060-005-4
 ; Sequence 4, Application US/11060005
 ; Publication No. US20050260693A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Irwin H. Gelman
 ; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
 ; FILE REFERENCE: A30558-A-FWC-A-A 070156.0597
 ; CURRENT APPLICATION NUMBER: US/11/060,005
 ; PRIOR FILING DATE: 2005-02-17
 ; PRIOR APPLICATION NUMBER: 09/902,432
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 08/978,277
 ; PRIOR FILING DATE: 1997-11-25
 ; PRIOR APPLICATION NUMBER: 08/665,401
 ; PRIOR FILING DATE: 1996-06-18
 ; PRIOR APPLICATION NUMBER: 08/635,121
 ; PRIOR FILING DATE: 1996-04-19
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 1596
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-11-060-005-4

Query Match 1.6%; Score 191.5; DB 7; Length 1596;
 Best Local Similarity 18.2%; Pred. No. 0.0047;
 Matches 320; Conservative 214; Mismatches 603; Indels 619; Gaps 83;

444 NEKAKDITDGGKINPKFVNSGGVVGSGGTSASGCTNDENKGTFTFSEVCGPCPDG 523
 109 NSTAVEDITKQOQEBTSEIE-----QIPSENVE-----EMVQPA----- 145
 524 VQHKGNQWERTKYKRWKSKLYKPIKNGKVLTKSLKLVND-----MMILKKNM 574
 146 -----ESQANDVGFKKVFKFVGPFT-----VKDKNKESPTVQLLVKQDE 187
 575 KEFCLTONSSDGSVG-----SVYT-TGASGG-NSEKKELDEWKCYKQNEVQKVVVG 625
 188 GE-----GABASVAGDHQBPSEVETAVGESASKESELKQSTKQEGTLKQSSSTEPL 241
 626 EYEDD---DDELKAGAGCLTLNPKKXKVS---EAKSQNHADLOKTHDFYI-WVAH 678
 242 QAESDQAAEEBAKDEG-----EKKQEKPTKSPSPSPVNSSETTSFKFETFGWAG- 294
 679 MLKDSIHRTKRLKSCISDGKTMKRCNGCNKCDCEKVVKQKETEMKPIKDHPTQDGI 738
 295 -----WRKK-----TSFK-----KSKEDDLETAERKKEQBAEKVDEBEK- 330
 739 PEGYFTTLELILKLOFLKEDTEENTENSIDAEBABELHLOKILKENENMLAVVNAQT 798
 331 -----TERASEBQEPALBDTDQARLSADYEK-ELPLEDQVGLBASS 371
 799 EOK-----TLMDKLANH-----ELNDATKCKDCPLPREDKSKRGRSAD----- 835
 372 BEKCKPLATEVEDEKMEAHQEVAAEVAVHSTVEK-----TEEOGGGGEAGGVVETGTS 427
 836 -PSPIFIPR--PEEKEDEN-----EDDDEBDVD-----DEETAKETEG--SAND 878
 428 LPPEKLAEPQVQEAPEALMLKSRKEMKVGSGDHTQLDLSPEKTLPKHEGGLVSEVE 487
 879 TTTSIDVCPVIGKVLTKDNESLQDACSLLKYGNNRSLGWRVCTPSEGEPTSSDKNGALCV 938
 488 MLSQERIKVQGSPLKK-----LFSSSGLK-----KLSGKKQKGRKGGGDBE 530
 939 PRRRLRLYIKKLVNDATKTESPOASGSEASSTSGSTTPPDSEKALIKAVESAALETFTL 998
 531 PEYOHIIH-----TESPE-SADEQKGSASSAPPEBT--TCLKGPLE----- 572
 999 WRYXEKKAVAOEGAGHGLPRVEBGSPEYDPEDKLKEGKIPDGFLRQWFY-----T 1050

573 -----APQD-----EABEGTTS-DGEKK-REGITPMASFKQWVTPKGRVRPS 614
 1051 LGDYRDLFSGSNDTTSVSKDTPSSNNLNKIVLLAGSTGEOBKRNKYEIGNPKRC 1110
 615 ESDKEEBELKYSATLSTDSIVSEMDEVKTV-----GEBQKEBEK-----RV 660
 1111 STERSAPVLVSHPQTMWENNGKYYHGWVCAVLTSSKDIKAGV-----EKKPOKIENPENLM 1166
 661 DTSVS-----WEALICGSSKKRARKASSSDDEGPRTLGGDSHRA 701
 1167 DEANKKPPPOYQYTNVXLNDSGTS--PRTT-QTQASSDNTPTTLTHFVKRPYFVFW 1222
 702 BEASK-----DKEAGDAVPASTQEDQAQSSSPBP-----AGSPSEGEV 743
 1223 BEWGSFGR---ERKKRLKQIKNDCKVNGDVRGSGGGEACDLSITHDYIVPSFNCG 1279
 744 STW-ESFRLVTPPRK--SKSLBEKABDSSVEQLSTEI-----PS 782
 1280 CGKHCSSYRKMI--ERKKIBFHKOS-----NAVGOOK 1309
 783 REESWVSIIKKEI PKRRKGRADGKQEQATVEDSGPVEINEDBNVAVPPLSEYNVEXK 842
 1310 TDATRNNGNT-----FDKEFCCTL----- 1328
 843 MEA---QGTTELPLQLLAGAVVYSEBELSKTLVHTVSAVIDGTRAVTSVEBSPSWISAVT 899
 1329 -----ETWPDAAKFLER--LKNQPCNKKEVGDD-----IDPEKDKTQH 1368
 900 BPLEHTAGEAMPVEVEVEKQIIAETPVLQTLPEGDADHDWTSVDFPSEAVLATE 959
 1369 TEYCGPCPKFTNCGNGCGVSGLNGCDDGDSIDAKEI--AKMSSTTDVYWRASDDT 1426
 960 T-----SEALTEVITASGAEBTTDVMSAVS----- 986
 1427 NTFEGDDLKACQAHANIFKGIKRDVWKCGVYCGVDICEQTNINERTDEKEYIQLRPFK 1486
 987 ---QLTSDPTTEATPQOEVESGVL-----DTEBEER-----QTQALILA 1024
 1487 WVENLEBYNNKINDKISHCICKGESSK---INGEKRSKCLEKKIEKKIEMWIKKRF 1543
 1025 VADKYKESQV---PATQTVOR-TGSKALEKVEEVESEVLASKEKDVMPKGVQEG 1080
 1544 NDQYENKQDPYNVKSLIEELIPKIAVNDQDN-----VYKL-----CVF 1583
 1081 ABHLAQSEITQATPESLE--VPEVTA--DVDHVAQCVIYKIQQLMEQAVAPESSETLTD 1136
 1584 ENSKGTLLISNT---QNNKENDALIDCMLKCLGVKAKNCPGRKSGEQSDCKEPPPLP-- 1637
 1137 SETNGSTPLASDPTADGTQOQBETIDSDQSKATAAVRQOQVTEEBAAATQKEBPSTLPNNV 1196
 1638 ---DEEDONPEBNTLEP----- 1651
 1197 PAQEBHEGEPGADVLEPQOELTAAVAVLAKTEVGOEGEVDMLDGEKVEBOEVFVHSG 1256
 1652 ---PKFCPTTQPREKGETGNKE--EKDQEKKESEBAPAKESGPAABEPAPTAESBE 1707
 1257 PNSQADADVTYDSEVMVAGCOEKESTVQGISLEEGEMETDVEKREKTEPEQVSBGE 1316
 1708 TETNPEBPPGT-----GPA--APPSTAPPTPTPTPPPLRQADBEFDTI 1750
 1317 QETAPABEHGTYGKRVLLDMWSSERKALDSIGSPFLPDDKAGCIEVQ--QSLDITV 1375
 1751 LQT-----TIPGVYALMGSI-----APFLKAKTKTASVGNLFOILOIPKSDYIPIFLK 1799
 1376 TOTAEAVKVIETVVISSETGSPBCVGAHLPAEKSSATGHW-----TLQ 1421
 1800 SSNRVIPIVVSRYKGYKTYIWMGDSDEDKVFAPMSPTTVNTSSSEB--YEELDINDIYVFGS 1858
 1422 HADTVPLGEPESQASSTIYIYTPAPESLHPDQO--EISASQRRSSEBDEPDGAD 1479
 1859 PKYKTLIEV-----LEPSGNNT-----ASGKNTPSDTRNDIQNDGIPS 1898

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Db      1480 GKESTAIEKVLKABEILLESESKNKIVLVNLTQVADQFARTETAPETHAVDSQTV- VPA 1538
Qy      1899 SKITDNE-----WNOLK 1910
Db      1539 CRLDSEPPRCWTMMK 1554

RESULT 7
US-10-793-626-1780
; Sequence 1780, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1780
; LENGTH: 1155
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-10-793-626-1780

Query Match      1.4%; Score 174.5; DB 6; Length 1155;
Best Local Similarity 18.7%; Pred. No. 0.026;
Matches 251; Conservative 140; Mismatches 492; Indels 459; Gaps 60;

Qy      1063 NDTTYSKUTPSSSNDNLK---NYVLASGSTEQER-EKMKYKXIKYKPKRST----- 1112
Db      56 NOLESAESKEOKSGSRNESSKLNQVLDLNGSHSSEKTTNNVNNATEKVKVEADPTSDVSKP 115
Qy      1113 -----ERSAPNLVSHPQTWENNGKYIWHGMWCAITLSKDKIAKVEKKPKIENPE 1163
Db      116 KANEAVNTHSTKPKTKTEAPV---NEESIAETPKTSTTQD---STRKNNPSLKDL 167
Qy      1164 NMDEANKKPKPPQYQYTNVKLDEN-----SGTSPRTQTOA---SSDNTPTTLTHF 1212
Db      168 NSSSTSKSKTDEHSTQAOQSTNKSNDLTNDSPTOSEKTSQANNDSIDNQSAPSKOL 227
Qy      1213 VRRPT---YFRWFEWGESFCREKRRK--QIKYDKVEN-----GDVGRCSGD 1257
Db      228 DKRPSEQKYKTKFNDPTQDVEHTTTTKLTPTSIDSSVNDKQDYTRSAVASLGVDSNE 287
Qy      1258 GEACDS-----ISTHDY-----S 1270
Db      288 TEAITNAVDNLDLKAASREQINEAIIAALKKDPSNPDIYGVDTPLALNTSOKSPHKS 347
Qy      1271 TVPSFNC-----PGGKHCSSYRKWIERKIEKIIEFHKOSNAYGOQKTDATRANGNTFDKEF 1324
Db      348 ASPBNMLMSLAEPNSGKAVNDKVK-ITNPTLSINKSN-----HANN----- 389
Qy      1325 CTKLETWPAAKFLERLKNQPKCTKNEYGGDDIDFKSKTQHTREYCP---CPKFT 1380
Db      390 ---VIMPTS-----NEOFNLKANYEILDSSIKSGDFTIKYGGYIRPGGLEPAIKT 437
Qy      1381 NQONGCGVSLNGNCDGKSIDAKRIAMRSSTTVWRVSD---NDNTPE----- 1430
Db      438 QLRSKD-GSIVANGVD-----KTNNTTTTTFNNYVDQYNTIGSPDLIATPKR 485
Qy      1431 GDDLKACOH-----AN-----IFGIRKDVVKCGVCGVDICEQTNINERTDGE 1476
Db      486 ETKAIKONQYPMVEVTIANEVKKDFIVDGNKKDNTTAAVANVD-----NVNNKNEV 540
Qy      1477 YIQIRALFKRWENFLIEDNKINDKISHCIKKGEGSKCINGCEKSKSCLEKTIKELIAM 1536
Db      541 YL-----NONNQNPKYAKFYSTVKNKFIPIG-----EVKVEV 573

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Qy      1537 ENIKRPNDOYENKQDPYNYKSIIEELIPIKTI-----AVNDQDNVYKLCVF 1583
Db      574 TDTNAMY-DSE-NPDLNNSNVKDVTSQTFPKVSDGTRVDINFAKSMANGKRYIVTQAVR 631
Qy      1584 ENSKGCFTLISNTQNNKENDALIDCMCLKGVAKKCPKPGSEKQSDCKEPPRLDDEQDN 1643
Db      632 PTGTG-----NVYTERWLTLDG--TTTNDPYRGTGKSTYTYLLNGSSSTAQDN 677
Qy      1644 PEENLT-----LEPPFCPTTPPEEKGETCGNKEKKEKESEREPKASESGPAEE 1698
Db      678 PTYSLGDYWLDRKK---NGVQDDDEKG--LAGYVYTLKOSNNNELQRTVTDDSGHYQFD 732
Qy      1699 PAPFAESEETETNPEPPGTPAAPS--TPAPTPPTPPPLRQADPEPFSTLQTTIP 1756
Db      733 -----NLONGTYVEFAIPDNYTPSPANNSTNDAI--DSIDERDGT----- 771
Qy      1757 FGVALALGSIAPFLFKKTKASVGNLPQIOLIPSDVIDPFLKSSNRITPVYSDRYGKT 1816
Db      772 RKVVYAKGTI-----NNADNMTVDGTF--YLTPTKYNVD 803
Qy      1817 YIY-----MEGSDSDKAFMS-----DT--TDVTSSESEYE-----ELD 1849
Db      804 YWEDTNKQGIQDNEKISVVKYTLKKNKNDITGTTTDSNGKYEFTGLENGDTIEFE 863
Qy      1850 INDIYVP-----GSPKPKY---TLIEVYLEPSGNNTASGNTP-----SDTRND- 1890
Db      864 TPEGTYFTKNSGSDGKDSNGTKTYTVKADNKTIDSGFYKPIYNLGDYWEDTNKDG 923
Qy      1891 IQND---GIPSKIT--DNEMNQ-----KKEFISNMQLONGNDVNDVDTSGNS 1934
Db      924 IQDSEKISIGVKKYTLKKNKNAIGTTTDSAGHYQFGLNNGSYTVEFTPSGTYTPKA 983
Qy      1935 STNTNITTSRHNVDNNTNTTMSRDNMEENLLPSIHGNIYSGEYSYNNVMVNSNDI 1994
Db      984 NSGQDIT-----YDSNGITTTGIINGADNLTI---DSGYKPKPKYSGVGYWEDTNKD 1033
Qy      1995 PINRDNNVSGIDLINDLSGKPIDYDEVYKREKNELFGTENTKRTSTONVAKTMSD 2054
Db      1034 GIQDDN-----EKISGVKYLKDEKNGIISTTTTD 1064
Qy      2055 PIHQLELFHKMLDRHRMCEKMKKEDILNKLKEWKNENINNSGKTYNSDNKPSHHV 2114
Db      1065 -----ENK--YQDNLDSGYI 1080
Qy      2115 LNTDVSIOQDMNPCKTEITNMDTQDSTWD-----TILDLEKYNDDPYVDYEDD 2168
Db      1081 -----IHFKEPKGMTQTANSQNDDEKADGSDVAVTITDHDHPSIDNGYFD--DGS 1130
Qy      2169 IYHDVVEKSGMDIYVDHNN 2190
Db      1131 DSDSDADSDSDSDSDADSDS 1152

RESULT 8
US-11-044-899-2
; Sequence 2, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Chen, M.
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51

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; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1163
; TYPE: PRF
; ORGANISM: Rattus sp.
US-11-044-899-2

```

Query Match	1.4%;	Score 170.5;	DB 7;	Length 1163;
Best Local Similarity	16.5%;	Pred. No. 0.044;		
Matches 160;	Conservative 110;	Mismatches 296;	Indels 401;	Gaps 33

Oy.		1619	PGKSGEGRQSDCKEPPPLPDEEDONKEENTLE-----	PKFCOP	165
Dd		18	PRPPPAFKYGVTEBEDEDEDEDEDEDEDEDELEVELEKKRPAAGLSAAAVPAAAAAP		77
Oy		1658	-----TTOPPEEKGETCG--NKBEKKDCKESEBEPKESGPAEBEAPTASBETE		1705
Dd		78	LDFSSESVFPAPRGFPLAAPPAAPERQPSWERSPPAABAPSLPAAAIVLPSKLPEDEBP		137
Oy		1710	TNPFEPBETG-----PAAPSTAPP-----	TPOTFFPLRPOA----	1744
Dd		138	ARPPPPPAGASPLAEPAAPSTPAPRRGSGVDETLLFALPAASEPVIPBSAEKIMDL		197
Oy		1743	-----DEPDSTILOTTIPFGVALAGSIAPFLFKKKTAYAGNLFOI-----		1785
Dd		198	MEQGNTVSSGOEPPSPVLLETASLPSLSTYSF-----KHNGYLGNLAVSSSBC		252
Oy		1786	-----LOIPK-----SDYDIPULKSSNRYPVSDBRYGKTYIWE		1822
Dd		253	IETLTNEASKELPERATNPFNVRDLAESELEYSEMGSFJKSP-----KGESALIYEN		306
Oy		1823	DSD-----EDKAFMSDTTDDVSS-----	EEX	1844
Dd		307	TKEEVIYRSKDKEDLVCSAALHSPQESPVGKEDRVASPEKTMIDINEMQMSVAVAREEY		366
Oy		1846	EEL-----DINDIY-----VPGPSKYKTLIEVLBPS-----GNNTTASG		1880
Dd		367	ADFKPFBAMEVKOTIBEGSRVDLARAAVAGESVODKCLDELSLEQSLOKDSGREDASF		426
Oy		1881	KNTP-----SDTRN--DIONGIPISSKITDNEMOLKKEFIEN-		1916
Dd		427	PSTEPEVQDSSRAYITCASFTSATTESTANTFPLEDHETSUKTEBKIEERKAQIIITEK		486
Oy		1917	-----MLONOENDVNDVTSGNSSNTNNITTS		1944
Dd		487	TSPTSNBFVAVQDSEADYTTDTLSKVYTEAAVNSMBGLPDLVOACBSLNATGT		546
Oy		1945	RHNVDNNTNTMTMSRDNMEENT-----LLPSIHGN-----		1974
Dd		547	KIAVETKVDLVOGTSEBIGESLYPTAQLOCPFEAEATPSPVLPDIWEAPIJMSLLPSAGA		606
Oy		1975	-----LYXGEYSYNVMNVANSMDIIPINKDNV-----		2002
Dd		607	SVPQVSPLEAPRPVSYDSIKLEBENPPYEAAVNVALKALGTKEGIKEPESFNAAOE		666
Oy		2003	-----YSGI-----DLINDSLGGKPIDYD		2022
Dd		667	TEAPYISIACLIKETKUSTEPSPPFSNYSELAKREKVPFHAEIJBESSPESBEVDLFS		726
Oy		2024	E-----VLKRKENELFGT-----	ENTK	2040
Dd		727	DDSIPVPOQOEAVMLMKESITLEVSEFVAHQIKERLASPOLGKPYLESFOPYLHSTK		786
Oy		2041	RTSQNVAKTNSDPRIHQLELFHKMRLDRHDMCKMKSKKDILINKLEBNKENINN		2100
Dd		787	DAASNDITLTKKEKISLOMBEFNFATISNDLL--SKKE--KIRE--SETFSSS		837
Oy		2101	KTYSNDKPSHHVLTANDVSIQIIDNDNKTKNETINMDTNODKSTMPTI-----LDLLE		2154
Dd		838	PIIIDEPTF-----VASAKDSPKLAKETYDLEVS-DKSIANIQSGADSLPCGE		887
Oy		2155	KYNBPYYDFPEDTIY--HDVDYKXSMDLIYUDHANNVTSNMDVPTROMIENKIYVANK		2212

Db 888 LPDLSFKNIYPPDEYHVSDEFSENRSSVSKASISPSNVSA--LEPQTEMG---SIYKSK 942

QY 2213 KEIFEER 2219

Db 943 SLTKAE 949

RESULT 9
US-11-044-899-30

```

1 Sequence 30 Application US/11044899
2 Publication No. US20050260616A1
3 GENERAL INFORMATION:
4 APPLICANT: Schwab, M.
5 APPLICANT: Chen, M.
6 TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
7 TITLE OF INVENTION: THEREON
8 FILE REFERENCE: 10200-017-9999
9 CURRENT APPLICATION NUMBER: US/11/044,899
10 CURRENT FILING DATE: 2005-01-26
11 PRIOR APPLICATION NUMBER: 09/830,972
12 PRIOR FILING DATE: 2001-09-24
13 PRIOR APPLICATION NUMBER: PCT/US99/26160
14 PRIOR FILING DATE: 1999-11-05
15 PRIOR APPLICATION NUMBER: 60/107,446
16 PRIOR FILING DATE: 1998-11-06
17 NUMBER OF SEQ ID NOS: 51
18 SOFTWARE: PasteSeq for Windows Version 3.0
19 SEQ ID NO 30
20 LENGTH: 1163
21 TYPE: PRT
22 ORGANISM: Rattus sp.
23 FEATURE:
24 NAME/KEY: VARIANT
25 LOCATION: (1)...(1163) at all Xaa position
26 OTHER INFORMATION: Xaa = any amino acid
27 US-11-044-899-30

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Query Match	1.48; Score 170.5; DB 7; Length 1163;
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Matches 161; Conservative 112; Mismatches 293; Indels 401; Gaps 34.

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Qy 1619 FGRSGRGSCKCPPLPLPDEEDONPEENTLE-----PKFCBP 165
Db 18 FRPPPAKYOFVTPEDDEDEDEDEDEDEDELELEVLERKPAAGLSAAVPPAAAAP 77
Qy 1658 -----TTPPEERKGETCG--NKEKKDEKKESEBPAKESGCPAAEAPTAESRETE 1706
Db 78 LLDSSSSVPPAPRGPCLPAAPPAAPERQPSNERSPPAAPAPSLPAAATVPLSLPDEDEBP 137
Qy 1710 TNFPEPPTG-----PAAPSTPAP-----TPDTPPLRPOA----- 1744
Db 138 ARPPPPAGASPLAEPAPAPSTPAAPRRSGSGVDETLPAAPASEPVIPSSAEKINDL 197
Qy 1743 -----DEPDDTILOTTIPFGALALGSIAFLFKKRTASGNLEQI----- 1786
Db 198 MEQDNTVSSQGEFPVSLLETAASLPBLSPLSTVSF-----KEHGYIGNSAVSSSECT 252
Qy 1786 -----LOIPK-----SDYDITLKSNRYIPVSDRYKGTIYMEG 1822
Db 253 IEEITLNAESKELPERATNPVNRDLAERSELFEYEMGSSPFGSP-----KQESALYEN 306
Qy 1823 DSD-----EDKYAFMSDITDVTSS-----ESRY 1841
Db 307 TKEEVIIVRSXDKEDLVCSALHSPQESPVGKEDRVASPEKTMIDIPNEMQMSVVAEVRBY 366
Qy 1846 EEL-----DINDIY-----VPSPKYKTLIEVVLBS-----GNNTTASG 1884
Db 367 ADPFPFOAMEVVKDTYEGSRDVLAAANVESKVRDKCLIEDSLLEKQSLGCKDSEGRNEDASF 426
Qy 1881 KNTD-----SPTRN-----DIONGIPSSK----- 1900
Db 427 PSTIEPVDKDSRAIYTCSFTSAESTTANTFPLLEDHTSENKXDEKILBERKAOIITEK 486

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QY 1901 -----ITDENMOLKEKIFISNM-----LONQPNVDVNDYSGNSSTNTTITTS 1944
 DB 487 TSPKTSNPLVAVQDSADYTTDTLSKYTEAAVSNMPEGTLPLDVQACSELINEATGT 546
 QY 1945 RHNVNNTNTTSSRDNMEENTL-----LIPSIHGN----- 1974
 DB 547 KIAYETKVDLVQTSSEAIQBSILYPTAQLCPSEFEAEATPSVLPDIWEAPLNSLPSAGA 606
 QY 1975 -----LYSGEYSYVNMVNMNMNDIPINRNNV----- 2002
 DB 607 SVQPSVSPLEAPPVSTDSITKLEPENPPYEAEANVAKALGTGKIGKESPFMAVQ 666
 QY 2003 -----YSGI-----DLINDSLSGKPIDYD 2023
 DB 667 TEAPYISACDLIKETKLTSTEPSPDFSNVSEIAKFEKSVPEHAHELVEDSSPESEVDFS 726
 QY 2024 E-----VLKKEHELGT-----ENTK 2040
 DB 727 DDISPEVQTOBEAVMLKESLJEVSEYVAQHKEERLASPOELGKPYLESFQPNLHSTK 786
 QY 2041 RSTONVAKTTNSDPIHNOLELPHKMLDRHDMCEKMKKEDILNKLKEWNKENINNSG 2100
 DB 787 DAASNDIPLTKKELISLOMEEFNTAISNDLL---SKED---KIKS---SETFSDS 837
 QY 2101 KTYNSDNKPSHNVLNTDVISIQIDMNPCKNEITNMDTNODKSTMDTI-----LDDLE 2154
 DB 838 PIEIIDEPFTF-----VSAKODSPRLAKERYDLEVS--DKSIAMIQSGADSLPCL 887
 QY 2155 KYNDYYIYDFEYDDIY--HDVDEKSSMDIYVHNNTVSNMVPFKHLENNIVNKK 2212
 DB 888 IPCDSFKNIYKDEHVHSDERSSSVKASISPSNVA--LEPQTEMG---SIVSK 942
 QY 2213 KEIFREE 2219
 DB 943 SLTKEAE 949

RESULT 10
 US-11-089-551A-30
 ; Sequence 30, Application US/11089551A
 ; Publication No. US20050266242A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lindquist et al.
 ; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
 ; FILE REFERENCE: 30554/40025A
 ; CURRENT APPLICATION NUMBER: US/11/089,551A
 ; CURRENT FILING DATE: 2005-03-24
 ; PRIOR APPLICATION NUMBER: US 60/559,286
 ; PRIOR FILING DATE: 2004-03-31
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 30
 ; LENGTH: 964
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 US-11-089-551A-30

Query Match 1.4%; Score 166; DB 7; Length 964;
 Best Local Similarity 19.3%; Pred. No. 0.061; Indels 120; Gaps 16;
 Matches 87; Conservative 69; Mismatches 175;
 QY 1780 GNLFOI--LQIPKSDYDIPTLKSSNRYIPVSDRYGKTYIYMGDSDEDKYAFMSDITD 1837
 DB 605 GLLFYIHEAQLPDKD-----SAREYDILKDAEGRSVLQLKDS-----MAASRT 651
 QY 1838 VTSSSEYEELDINDIYVPGSPRYKTLIEVLIPSGNNTTASGKNTPSDTRNDIONDGI 1897
 DB 652 YMLNQLIPEKLN-----SKTIQTALHSSPSNESAFLVTNNSALKPHLGDSIQ 700
 QY 1898 -----SSKTDENMOLKKEFISNMLOQNPVNDVNTYSGNSSTNTTITTSRHVNDNT 1952
 DB 701 PVFVSSQDTKQSFSLAKSE-----ESTNDYAMANYLNTNPIS-----ENPL 742

QY 1953 NTTNSRDNMEENTLIPSIHGNLYSGEYSYVNMVNMNMNDIPINRNNVYSGIDLINDS 2012
 DB 743 NEAQOQOVQSG-----TTMSN-----ERPNNFLSILIRDN 776
 QY 2013 LSGKPIIDIVELVKE-----NELPQTEKTSIQNVAKTNSDPIHNOLELPHKML 2067
 DB 777 NGQSNILDAFDVIRNDGDIPTNSAFDPSSK---SNASNSNPDTINN----- 823
 QY 2068 DRHDMCEKMKKEDILNKLKEWNKENINNSGKTYNSDNKPSHNVLNTDVISIQIDMDN 2127
 DB 824 -NYNNVSGKNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 870
 QY 2128 PKTYNEITNMDTNODKSTMDTIILDDLEKNDPYIYDFEYDDIYHDVDEKSSMDIYD 2187
 DB 871 GNSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 918
 QY 2188 HNNVTSNMDVPTKQHIEMNIIVNNKEIFEE 2218
 DB 919 DKEMSPRIETIKNEON--MTDSNDILGVFDQ 947

RESULT 11
 US-11-013-759-11
 ; Sequence 11, Application US/11013759
 ; Publication No. US20050249747A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Locomore, Sheena M.
 ; APPLICANT: Sasaki, Ken
 ; APPLICANT: Yang, Yan Ping
 ; APPLICANT: Klein, Michel H.
 ; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
 ; FILE REFERENCE: 1038-921MIS:jb
 ; CURRENT APPLICATION NUMBER: US/11/013,759
 ; CURRENT FILING DATE: 2004-12-16
 ; PRIOR APPLICATION NUMBER: US/09/361,619
 ; PRIOR FILING DATE: 1999-07-27
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 2314
 ; TYPE: PRT
 ; ORGANISM: Moraxella catarrhalis
 US-11-013-759-11

Query Match 1.4%; Score 164.5; DB 7; Length 2314;
 Best Local Similarity 17.9%; Pred. No. 0.022;
 Matches 428; Conservative 249; Mismatches 778; Indels 931; Gaps 109;
 QY 17 HVLDEFQKRVHDEVHGEAKNYVELKSLASLIGETAFYVKSMTESKTELEANSK 76
 DB 215 HFANAFGR-----STAEQVSLA--VGLTA-----KAKGYTIALGSAQ 253
 QY 77 RNPCKGDKGND--VDRSVKQNGYDNKKKKCSGMCAPFRRLHLNKNPFMNSNDS 134
 DB 254 AINYGALALGADTRD-LDYGIALGYGQIL-----NNNNNNN 290
 QY 135 SKAKHDLAIVCAKAYEGESIKTHYPKYDSKYPSPDMCTMLARSPADIGDIIRGDL 194
 DB 231 NKA-----YPEEGNGSNKS-----SKATONGL-----PSISSTIKRKII 326
 QY 195 YLGNKKKKONGKETERELKLEIKFPIKHIDNLKDKAQRKNGDEDPNFKLRBDWMT 254
 DB 327 NVG-----AGVEDTDAVVAQ-LKAV-----ENLAKR--QITFKGDMDGTGVKKK----L 369
 QY 255 ANRETVKAMTCSKEL-DNSSTFRATCNDTG-----GQPSQTHNKRCDXK----G 301
 DB 370 GETLLIKGEGTQADLTNNNIGVVTDNNTGLKYGLANLSGLFVSTNLTASAKVTYG 429
 QY 302 ANAGKPKAGDGVTVTPYFDVPOYLRFEFEMADFCRKKKKKLENEKQCRGKQKSD 361
 DB 430 SGNNTAEILOSGLITFTPT-----TNASIDKTYVG---IDG 461

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QY 362 YRYSRNGYDEQOTISRKGVNMG---KGCTDCEFFAGSYEN--WIDNOKQDFDKOKY 415
DB 462 LKFTDNSTWTALEDT--TRITKOKIGSNKAGTVD-----ENKRYLXK-----DKLKV 507
QY 416 TKEISDGGGRKRAVGGTTKYEGYKSFYEKLANDGYTDAFGLLNNK--ACDITD- 473
DB 508 NSTLNNGGILVNNITIGGSNK-----QIQVAGAGIKFADVNVVNSNAKGTTRITBE 559
QY 474 -----GGKI-----NFKVNSGGGVGGSGSGTSG-----ASGTNDENKGTFR 512
DB 560 EIGFADADGKVKDKSPYLDKKQOVGVKITKOSGINAGDQKISNVKQATDTDVATYKQ 619
QY 513 SEYCCPDCGVQHKGNQMERKTVKQKRWMSLYK-----548
DB 620 LKQVQDADGALQSS-----TRDEKGGFETISNLSNGNTPTFTITPAGENGISISND 675
QY 549 -----PINGRW--LILKSLKVVYKDMILK-----N 573
DB 676 IAKGVKVGIDPINALTPKLTGSDKDGKTQVIEQVASGNDTRNIIIRGLSPTLSITN 735
QY 574 WKEFLTQ-----NSSDGSVGSVTTG-----ASGNS 602
DB 736 AGGVRTTQGNITTSDEDKSKAASIGDILNTGFNLKNNNSVGFVSTYNTVDFIDGNAT 795
QY 603 KEELYDEWKCYKHNVOKVNVQGEVEBDDDLKAGGLCILPNPKNKEVSEAKSQNNHA 662
DB 796 AKVTYDE-----TNGTSKYTVYVNVDEKTIELTGNG-----KTNK----- 831
QY 663 DIQKTFHDFYYVVAHMLKDSIHMTKRLKSCISDGMTKCRNGCNKKCDCEKVKVKE 722
DB 832 -----IGVKTITLTNNAGKATNFTSTDN-----DALVNAKD 864
QY 723 -----TEWKPDKHFKTQOEGIPBEGYFTTLELILKQLKEDTEBNTENSIDABEAEHLKQ 780
DB 865 IAENLNTLAKELHTTKG-----TADTALQTFYKKGATDITDITVVGKGTNGKTV 916
QY 781 KILKLENNENLAVNVAAGTEOKTLMKLNHELNDATKCDPLPREDKSRGSADSPD- 839
DB 917 NTLKLGKNGLTVA-----TNKDGTVTFGINTOSGLK-----AGDSTTLNKG 959
QY 840 IFIPPEEKEDENEDDEDEVRDEETAKETTESATDTTSLDVCPIVKV-----L 893
DB 960 LSIKRPASNEQIOVGADGVKFAKVDKNSSTGIDGTSRITKQOIFGTANGSLDITTKPHL 1019
QY 894 TKDNESLQDASLKG-----GNNSRLKRCVMT--PSGERTSSDKGKAIQVPPRRR 944
DB 1020 TKD-----KLKVGVEITNTGINA--GGKKITNIOGDTTQNS--NDAVTG----- 1061
QY 945 LYIKKIIVMATKTESPOASGSEASSTGTPPDSKALKAFAVESAMIEFFLWHRKE 1004
DB 1062 ---GKVVYDKTELESKINSAAKTAQNS-----LHER-- 1089
QY 1005 EKKAVAGEAGHGLPRVEGSEPEYDEPKLKEGKIPDGFRLQMFYTLGDYRDLIFSGND 1064
DB 1090 ---SVADQGNHFTV-----SNPYSYDTSKTSV-----ITFAGENG 1124
QY 1065 -TTSVSKQTPSSSNDNLKNIYLLASGSTBOERERKANKYKIKNFKKSTERSAPLVSH 1123
DB 1125 ITTKVKNKVVRVGDIDQTKL-----TTPPL----- 1149
QY 1124 QTMENNENKTYIWHGVNVALTSKDKIAKGVKKPKIKENPENLMDANKPKRPQOYTNN 1183
DB 1150 -TVGNNGKGI-----VIDSD----- 1165
QY 1184 KLDENSGTSPRTTQOASSDNTPTLTTHFVKAPTYFRWFEWGESFCEKRRKRLKQIKVD 1243
DB 1166 ---GGTITIGLSWTLANTNDAGHALSGLANDT-----DKTRAASI--- 1205
QY 1244 CKVENGDV---GRCSGDEACDSISTHDYSTVPSFNCPCGCKSSYRKMIERKIEFH 1299
DB 1206 ---GDVLNAGFNLONGEAVDFSTYD----- 1229
QY 1300 KQSNAYGOQKTDATBNNGNTFDEKFCITLETWPAKFLERLKNKPCCKTNKEYGDDIDF 1359

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DB 1230 -----TVDFIDGNAT-----AKVYDDTS-----KTSKVV-----YDV 1258
QY 1360 EKDKTPQHTREYCGPCRFKTNQNGNGVGLNN-----COGDKSIDAKKELAKMSS 1413
DB 1259 NVDNKTIETEVTS-----DKKIGVKTITTYKTSANGNATKPSAADBALVAKSDIA----- 1307
QY 1414 TTDVVRVSDNDTTPBEGDILKDACOHANIFPKGIRKQDVWKGVYGVVDFICEQTNINERTD 1473
DB 1308 -----THMLTLAGD-----IQTKAGASQASASASY-----VDADGNKVIYDSTD 1346
QY 1474 GKEYIQIRALFKRVNENFLEDYNNKINDKISHCIKKGSSKINCCEKSKLEKIEKTI 1533
DB 1347 KK-----YQVNDK-----GQYDKKKEVAK-----DKLV 1370
QY 1534 AEMENIKRFRNDQYENKQDP-----YVKSILBELPKIAVNDQDVIVILCVFENSKG 1588
DB 1371 AQAQT-----PDGTLAQNNAKSVI----- 1389
QY 1589 CTLSINTQNK--NDALDCLKLGIVAKKCPGKPSGKQSDCKEPPPLPDEBDQNPBE 1646
DB 1390 -----NKGQVND-----NKGQINEDNAFIKGLENAKDTTKRAATVGBLNAVA 1436
QY 1647 NTLBPKECPPTQPPBE-----KQGETCGNKEKKDKBKESEBPKEGPAEAP 1699
DB 1437 QT--PLTFAGDGTAKKLGSETLTIKGGQDTNK-----LTNNIGVAVGTD 1481
QY 1700 APTASEETENFPBPGTGAAPSTPAFTPTPTPLRQADPEFPSTI-----LQ 1752
DB 1482 GFYVLAADLTNLSVNAAG-----TRIBEKGISFVANGAQAKAN 1521
QY 1753 TTFPGVALAGSIAFLFLKKTAKSVG-----NLFOILOIPKSDYDIPTLKSSNR 1803
DB 1522 TPVLSANGLDG-----KRIISITGAAYDNDADAIVFKQPNBAKTVNNLNNOSNGA 1573
QY 1804 YIPVSDRYKKTYYIMEGSDDEKTAFAWSDTTDVTSESEYEELIDINDIYV--PGSP-- 1859
DB 1574 SLFPVYVDANGKP--INGTDGKPKQA-----IKGADKXYHANANGVFPVDKGKPYT 1623
QY 1860 ---KKTILI-----EYVLEBSGNNTTASGNTTS-----DT-----RNDIQNGI 1896
DB 1624 DADKLANIAHAKPLDACHQVVASIGNSDAITLTINISTLPQIDTPYTGANNAGQAQSL 1683
QY 1897 PSSKITDENVNQLKEEFSNM---LONQPN--DVNDVTSGNSSTNTITTSRRANVN- 1950
DB 1664 PSLSAAQOS--NAAKYVDLNVGFNLQTNHNOVDYKAYDITVNFVNGTADITSVASADGT 1742
QY 1951 ---NTNTMSRDMWENLILPSIHDGNYGSEBYSYVNVNWNVNSMNDIPINRNNVYSGI 2006
DB 1743 MSNITVNTALATDDGAVILKA--KDGKFFYADDLMPV-----GSLKAKSASDAKTPPGL 1797
QY 2007 DLINDLSGGKPID-----IYDEVLKXKENELFGENTKRTSTONVAKTNSDPFHQL 2060
DB 1798 SLVNPNAKSGSTGVALNLSKAVFKSKD-----GTTT-----TVSSDLSISIO- 1842
QY 2061 ELFHKMDRHRDMKEMKMKEDILINKLEBNNKENINNSGKTVNSDNKPSHNHVLNTVS 2120
DB 1843 -----GDNSSI-----TISKQGLNAGVYISVNGKGYD----- 1872
QY 2121 IQIDMNPXTKNEITNM-----DTNOKSTMDTITLDLEKYNDP 2159
DB 1873 --TDAAVQQLNBYRNLGLGNAGNADNAGQVN--IADIKK--DP 1912

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RESULT 12
US-11-089-551A-35
; Sequence 35, Application US/11089551A
; Publication No. US20050266242A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al.
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40025A
; CURRENT APPLICATION NUMBER: US/11/089, 551A

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US-11-089-551A-35

;; ORGANISM: Saccharomyces cerevisiae
;;
;; TYPE: PRY
;; LENGTH: 454
;; SEQ ID NO 35
;; SOFTWARE: PatentIn Ver. 2.0
;; NUMBER OF SEQ ID NOS: 65
;; PRIOR FILING DATE: 2004-03-31
;; PRIORITY APPLICATION NUMBER: US 60/559,286
;; CURRENT FILING DATE: 2005-03-24
;;

Query Match	1.4%;	Score 164;	DB 7;	Length 454;
Best Local Similarity	21.2%;	Pred. No. 0.03;		
Matches 96;	Conservative 76;	Mismatches 163;	Indels 118;	Gaps 23

Qy	1773	KKTKASVGNLQIILQIPKSDIDIFLTKASNRIRIPVYSRQKQTYI-----Y	181.9
Db	72	KKSKRSANSM-----NDKK--KCRITTKDM-----TRDSKQVTKMDHAKASHSMKY	117
Qy	1820	MEGSDDEDEKVAFMSDTPVTSSSESEYEELDIN-----DIYVGSBKTYLIEVLEPSGN	187.4
Db	118	KKRSYDCKH--VMKODSIVKASKNMSHNYSTJTNMKMDVYTKANANKKSDPTWKKNK	175
Qy	1875	NTTASGKTPSPDTR--NDIONDGIRSSKITDNEMWQLKKEFI SNMLONQPNVPDPYTSG	193.3
Db	176	KSHVSYNNDKSTKTKYNDSDD--DDNNVNNNDN-----NNKKNDDNNNDNTSN	225
Qy	1933	NSSTNTNITTTSRHNVNDNNTN--TTMS--RDNMENELLPISHDGNLYSGEYSYNNVNV	198.8
Db	226	NNNNNNNTKNNRRNRNRDMKTKCTDMNDGRDNNKNDM--AANDHKNTN-----NVNKR	277
Qy	1989	NSMNDPIPNRDNNTVSGIDLINDISLGGKPT--DIYDEVILAKRENELFGTEKTRISTQNV	204
Db	278	NHKS--CRDQ--YSANNAVSTASKNQVNDMNDNYKNTDITNNKNDSSNDVTRK	333
Qy	2048	AKTNSDPIHNDLELPHKWLDRHRCMEKMKKEDILNKLKEENKKNENINNSGKTYSDN	210.7
Db	334	RKTSBGNTSRNNVS-----VRSKATTKTKKK-----KRGQDKKN-----KKMADN	377
Qy	2108	KPSHNHLVNTDVSIOI--DMDNPKYKELITNMDTND--KSTMDTILIDLEKYNDDPYDYF	216
Db	378	KK-----NNAVTVSYDSDNKKYSNKRSRKANKKSDVNVSGKDSVKSCKKYAD-----	425
Qy	2165	YEDDIYHDVVEKSSMDIYDHNHNVNSNMD	2197
Db	426	-----NNTKSNDD	434

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RESULT 13
US-10-485-517-129
Sequence 129, Application US/10485517
Publication No. US20050256299A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biogenexus Incorporated
APPLICANT: Foster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629MO
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: PatentIn version 3.1
SEQ ID NO 129
LENGTH: 895
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-485-517-129

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Query Match 1.3%; Score 163; DB 6; Length 895;
Best Local Similarity 19.6%; Pred. No. 0.08;
Matches 141; Conservative 101; Mismatches 262; Indels 216; Gaps 377

Qy	1552	QPOVNVSLIEBELLPKIAVNDONVXKLCVFNSSKCTILSN-TONNKEDADIDCMUK	1610
Db	221	KPIINDPSLVKSDTNDNAVVTNDOS	264
Qy	1611	LGVAKKCPCKPSGKSDCKEPPPLDEBDONBEENTLEBPCKPEPTTOPPEEKGETC	1670
Db	265	-----NANNOQ-----QATNMOSQPAQPKSTANDQ-----ASSQAHETNSN--	303
Qy	1671	GNNKEKDOEKESSE-----EPAKESGPAAEPAAPAESHEFTTNPEPPGCTOPAAPPS	1725
Db	304	GNTMDKTNSSNGSDVANOQYPPADESLQDAIKNPA-IIDKSHTDNM-----	349
Qy	1726	TPAPEPTDTPPLRPQADE-----PPDSTLOTTIPGVALALGSLAFLEKKTASYV	1779
Db	350	-----RPIDFQMKNDKGERQFYHASYVEPATVIF--TKTGFILGLK--TJST	395
Qy	1780	GNLFQILOIPKSDYDIPFLKSSNNYIPVSDRYKGYI-----YME	1821
Db	396	WKKEVEY--GDKKLPV-----ELVSDSD--KDYAIRPVSNGREVIVSIEGE	445
Qy	1822	GDSDEDDYAFMSDTTDTYSSSEXY---EELDINDIYVPGSPRYTL-----IEVLEPS	1872
Db	446	NIHEDDYITLWFAQPIITNNPDYVDEBTYVQLGLAP-YHAKITLERQVLEYLEQEL	504
Qy	1873	GNNTTASGKNTPSDTR-----NDIONGIPBSKITDNEMOULKEFISMLNOQ	1921
Db	505	PEKYAEKPKKLDQTRVELADQVKSAAVTEFENVPITNDOLTDQ---BAHFV--VFESSE	558
Qy	1922	PND-----VPNYTSGNSSTNNITTTSEHN-----VDNNTNTTMSHD--NMEENTL	1965
Db	559	ENSSESVMGFEHFPYATTLNGQKYVNMKTODSYMKDLVSGKRYTVSXDOPKNSRTL	618
Qy	1966	LLPSIHQNLVS-----GEESYXVMNV--SMNDIPINRDN-----NYS9S--	2005
Db	619	IFPITPDKAVYNALVYVVANIGVEGQYHVAIINQDINTKDDPSQNNTSSEPLNVQGOE	678
Qy	2006	-----IDLINDLSGKPIDYD--EVLKRENELFTEGTEKISTONVAKTNSDPLHN	2056
Db	679	GKAVADTVAENSSTATNPKASDRAVDIPESDVDKADN-----NIDKVOGD--	727
Qy	2059	QLELFHKLLDHRDMC-----EKAKNKE---DILNKLKEBNKNENNSGTYVSDNKS	2110
Db	728	-----VDHLSDMSDNNHFDKDYDKEMDQIADKTDRANVDKADNSVSGMSNVDTXQ	779
Qy	2111	HNHVLNTDVGSOI-----DMDN-----PKTKBEITMMDTNODKSTYDITLIDLEKYND	2158
Db	780	SNK--NKOKVLOLNHIAKNNHNTGKAALDVAVKONNTNTDKYTKTEHLEPSDHLKTYD	837

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RESULT 14
US-10-995-561-773
; Sequence 773, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 773
; LENGTH: 3803
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-995-561-773

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Query Match 1.3%; Score 162.5; DB 6; Length 3803;
 Best Local Similarity 17.2%; Pred. No. 0.53;
 Matches 328; Conservative 261; Mismatches 698; Indels 623; Gaps 89;

8 GGTODEADAKHVIDEFGQKVHDEHGEAKYSELKGSLSIASILBETAFTVKSMOTESK- 66
 1844 GSSSPETLPILLKROGSFSED-----VISHKGDLRFVTISGQKVLDMENSKEGKE 1894

67 -----YTELLEANSKRNPKCKXK-----GNVDRFSYVE 96

1895 PSEIGNLVKDKLKDATERYTA-----HSKCTRLGSHLMLLGOYHOFQNSADSLQAM 1948

97 QAGYDKMKKCSNGMTCAFRRLHLCKNKPNNNSDSKAGDILAEVCMA-----KY 151

1949 QACEANVELSLDPTASDP-----GVLOBLATTKQLESLAHQVPELQGVARDIMEI 2004

152 EGESIKTHVPKYDSKYPGSDPFMCWMLASPADIGDIIRGRDYLGNKKKKONGKETERE 211

2005 EGEPAPDH--RHVQETTSILSHFQSLSYSLAERSSIL-----QKALAQSQSQVE 2052

212 KLEQLKELFKKIHNLMDKEAKRYNG--DEDNPFYTLRED-----WMTANETV-- 260

2053 SLESLLQSI-GEVEQNLREGQVSSLSGVIOEALATNMKLKODIARQKSSLEATEMTVR 2111

261 -----WGAMTCSKELDNSSYFRATC-----NDTGGQSPQTH 291

2112 FMETADSTTAVALQGLAEVSRFEOLCLOQOEKSSLKLLPQAMFPHLSGKLOQPM 2171

292 NKCRCDKDGANAGPKAGDGVITVPTVFDYVPOYLWFE----- 333

2172 NKSR-----MLASGNP--DQDIT--HFFQOIQELINLEMEDQOENLDTLEHLVTELSG 2221

334 -MAEPFCRKKKKLENLEKQCGKXKSDERYCSNRNGDCEQTIIRKGVNRKSGCTDCE 392

2222 GPALDLC-OHQRVONLRKDPTELQKTVKER--EKDASSCOQLDEFRLL----- 2268

393 FACGSEYEMWIDN-----QRKOPDKOKYTKKESIDGGRKKRAVAG--TTKYEGY 439

2269 --VRFFQKMLKETBSIPTETSMASKELBKQIBHKLSLDMASKGLTVEINCKGISTL 2326

440 EKSPYEKLNKNDYG-----TVDAFLGLANNEKACKDIT--DQKINFEVNSGGGV 488

2327 ENLIMEITAPBQKGTGSLPBGVSSVGVNGYHCKDLTEIQCMSPVNLKYKELG--- 2383

489 VGGSGGGSIGASGTNDENKGTFRSRYCQPCPDQYQHKGNQMERKTKVKKM--RMSGL 546

2384 -----GVLH-----BROESLQALINRMEEV 2403

547 YKPIGKNVLLKSLKVVKNMMILK-----KMKKEFC--LTONS-----SDG 586

2404 HKEANSVLQWLESKEEVLKSMAMSSPTTETVKAQAESNKAFLEBLEQNSFKIQKVKA 2463

587 SVGSVVT--TGASGNSSEKELYDEWKCYKHNVEQATYVQGEVEEDDELK----- 635

2464 LAGLLVTPNQSQAENMKKIOEILNSRME--RATEV-TVARQQLSEASHLACFOAAS 2520

636 -----GAGLCILPN--PKNKKEYS-----EAKSQNNH----- 661

2521 QLRPWLMEKELMMGVGLPSLIPNMLNQOQVQFWLKEFEARQOHEOLNEAAGILNG 2580

662 -----ADIOKTFHDFYVVAHMLKDSIMHRTKRLSCJSDGTMKCRNGCNKKDC 713

2581 PGDVLSTISQVKELOSINQKWE--LTDKLSRSSQIOAI-----VKSTQ 2625

714 PEKWKQKETEWPKIDHEKTOEGI--PEGYFTTLELILKLOFLKEPTEENTENSIDA 770

2626 YGELLQDISEKVRAGQRLSVQSAISTOBEA-----VKQLESTSEIRSDL 2671

771 EBAE-ELKRLQKILKLENNMLAVNAGTEQTLMDKLNHMLNATKCKDPLB-BEK 828

2672 EQLDHEVKAQTLG-----DELSTV-----IEQYLYKDELKRLLETVALPLQGLEBL 2718

829 SNGR-----SADPSPDIFIPREBEKEDDENEDDEBVR--DDEETAKETTESGA 876

DB 2719 AADRINRLQALASTQOFGQMF-----DELRITWLDKQSQQAAN----- 2757

QY 877 TDTTSLDVCIPVGV-----LTKHNESLQDACSIXYGGNNSRLGMRCTPGEPTTSSD 931

DB 2758 -----CPIASLEILQSOLOENEFQKSLNHSG-----SYEVLVAGEBSLLIS- 2801

QY 922 KNGAICVPP--RRRLYIKIYDMATKTESPQASGSEASTSGSTTPPSKEALLKAFVES 990

DB 2802 -----VPPGEKRTLQOLQVELKNHMBELSKTRDROSR-----LKDMQRLAQKQ 2847

QY 991 AAIEPFLMRYKEBKKAVAQAGAGHGLPVEEGSPEDP--EDKLEKGI PDGFL--- 1044

DB 2848 WHVEDLVPM-----IEDCKA-----KMSLEKVLTDLPVQLJESSLRSKAMLEVEK 2893

QY 1045 ROMFTYLDYDILFSGSNDTTSVSKOTPPSSNDLXKI---VLAASGTBEREKMKY 1101

DB 2894 RSLLEILNSAADILINSSEADEGIRDEKAGINQMDAVTEBLQAKTOSLEBMTQRLNEF 2953

QY 1102 KE-LKNFRKCSSTERSAPMLVSHPTWMENNGKIWHGWCA-----LTSKDIKAGYVK 1154

DB 2954 QESFNIRK-KVEGA-----KHOLEIPDALG-----SQACSKMLKELRAQOEVLOALEP 3002

QY 1155 KPQKLEN-PENLMBEAN-----KKRPQOYQYTNVCLDENSSTSPRTTQOASSDN 1204

DB 3003 QVDYLRNFTQGLVEDAPGSDASQLLHQAEVAQGEFLBYQVRVNSGC-----VMMEN 3054

QY 1205 TPTTLTHVVKPTTYFRWFEENGESECRERKRLKQIKYDKRYEN-GDVGRGSG----- 1256

DB 3055 K-----LEGIQGFHCRVREMFSQLADIDDELIDGALGRDLSLOQIE 3098

QY 1257 -----DGEACDSISTHDYSTVPSFNCPSG-----CGKHCSSRYKWIERRK 1295

DB 3099 DYRLFLANKIHVLKLDIEASEBACRMLEBEGTLDLGLKRELEALNKQCG--KLTERRK 3155

QY 1296 IEFHKNASVAGQOKTADTRNNGNTEPDKFCCTLFTWPAKFLERLKNGPCKTNREYGD 1355

DB 3156 AR-----QEOLELTLGRVEDFYRLG-KGLNDATTAAEBEAL-----QMVVGT 3197

QY 1356 DIDFEK---DSKTFQHTYEGCPCEPKFTNCONG-----NGVSGLNGCDDGK 1400

DB 3198 EVELIINQOLADFKMQO-DEQVDP-L-QMKLQOVNNGOGILQISAGKDCVQGLEH----- 3249

QY 1401 SIDAKEI-AKRRSSTDYVMBVSNDVNTVTFEGDDLKDACQAHNIFPKIRKOV--WKCGV 1457

DB 3250 --DMEELNARMWTLKKAQORLA-----QLOEALLHCGKFQDALBPLSLMAD-- 3295

QY 1458 CGVDICEQTNINERTDGKEYIQIRALF--KRWVENFLBYDYNKINDKISHCIKKGSGSKI 1515

DB 3296 -----TEELIANQKPSAEYKVVKAQIOEQKTLQRLDLDRKATVWML-----QABGGRIA 3345

QY 1516 NGCEKNSCKLEWIEKTAEMENIKGRND-----QYENKQDPY 1555

DB 3346 QSAELADR-----EKIQOLESSLESRTWTELLSKAABOKOLEDLVLAKQPHETAEPLS 3399

QY 1556 NVKSLLEELIRKIAVYNDQDNVYKLCVPENSGCTLISNTONKENDAID 1605

DB 3400 DFLSTVEKKLANSEPVGTQAKIQOQITRHRK-----LEEDINHAHTD 3442

RESULT 15
 US-10-995-561-771
 ; Sequence 771, Application US/10995561
 ; Publication No. US20050272054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 ; TITLE OF INVENTION: DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01559
 ; CURRENT APPLICATION NUMBER: US/10/995, 561
 ; CURRENT FILING DATE: 2004-11-24
 ; NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 771
 LENGTH: 3960
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-10-995-561-771

Query Match 1.3%; Score 162.5; DB 6; Length 3960;
 Best Local Similarity 17.2%; Pred. No. 0.56;
 Matches 328; Conservative 261; Mismatches 698; Indels 623; Gaps 89;

8 GGTODEDAKAVLDFGQKVDHVEHGAANYVSELKGSLSLSIGETAFYTKSMQTEK-66
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 67 -----YTELLEANSKRNPKCKDKG-----GNDVRFYSYKE-96
 1895 PSEIGNLVKDKLKDATERYAL-----HSKCTRIGSHLMLLQGYHQFQNSADSLQAM-1948
 97 QAGYDNKMKKCSNGWTCAPFRRLHLCKNRPNNNSNDSSAKHDLLAEVCAA-----KY-151
 1949 QACENAVKSLSDPTVADSP-----GYLQGLATTTQLOELABHQVPVEKLOKVARDIMEI-2004
 152 EGESIKTHYPKYDSKYPSDFPMCTMLARSPADIGDITRGDLYLGNKKKQNGKETERE-211
 2005 EGEPAEDH--RHVQETTSILSHFQSLSYSLAERSSLD-----QKAIAOSQSVQE-2052
 212 KLDEKLEKIFKKIHNLKDKAOKRYNG--DEDPNFKLRBD-----WMTANRETV--260
 2053 SLESLLOSI-GEVEONLEGVKOVSSLSGVIOBALATMKLKDILAROKSSLEATREMYTR-2111
 261 -----WGAMTCSKEIDNSSYFRATC-----NDTQGGPSQTH-291
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 2172 NKSR-----MLASGNP--DDIT--HFPOQIOELNEMEDQENLDTLHLYTELSSC-2221
 334 -MAEDPCKKKKKLEKQCKGCKDSBYRCSNGYDCBETIRKQKVRMGKGCCTDCF-392
 2222 GFALDLC-QHODRVONLRKDLFTELQTYKER--EKDASSCOEOLBEFKL-----2268
 393 FACGSYENMIDN-----ORQPDFOKKYYKEISDGGGRKRAVAG-ITKYEGY-439
 2269 --VRFOQMLKETEGSIPPTETSMASAKLEKQIEHLKSLDDMAKGLTLVEINCKGSL-2326
 440 EKSFYEKLNDYG-----TVDAFLGLLNNEKACKOIT--DGKINFEVNSGGGV-488
 2327 ENLIMEITAPDSQGTGSLPESVGSVSVNGYHTCKDLTEIQCDMSVNLKYERLQ---2383
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 2384 -----GVLLH-----EROSLOKAILNRMEEV-2403
 547 YKPIKGKVLILSLKLVVNDMMILK-----KNWKEFC-LTQNS-----SDG-586
 2404 HKEANSVQLWLESKEVLEKSMQANSSPTTETVYKQASBNKAFLELBQNSKIKQYKXA-2463
 587 SVGSVVT-----TGASGNSEKELYDEMKCYGHNEVQKYNVQGEVBEDEDLK-----635
 2464 LAGLIVTPNSQEAEMWKIQEELNSRME--RATEV-TVARQROLESASHLACFOAAS-2520
 636 -----GAGGICILPN--PKNKKEVS-----EAKSONNH-----661
 2521 QLRPMLMEKELMVGVLGPIIDPNMLNAAQOVQFMALKEFARRQOHEQLNPAAGILTG-2580
 662 -----ADIOKTFHDFYVVAHMLKDSIMHRTKLSKISDGKTMCRNGCKKDC-713
 2581 PGDVLSLSQVQKELQSIQKVE--LTDKLSRSQIQOAL-----YKSNQ-2625
 714 FEKWVQKQETEMKPIKDHFKTQEGI--DEGYFFTLLEILKLQFLKEDTEENTENSIDA-770

2626 YQELDQLSKRAVAGRLSVQSAISTQPEA-----VKQGLEETSEIRSDL-2671
 771 EEAE-ELKHLQKILKLENNENLAVVNAQTEQKTLMDKLLNHELNDATKCDCLPE-BDK-828
 2672 EQLDHEVYKQATLTC-----DELSTV-----IGEQYLKDELKRLLETVALPLQGLEDL-2718
 829 SRGR-----SADSPDIFIRPREKEDDEDEDDDEVR--DDEETAKETTESA-876
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 2802 -----VPGEKERTLQNLVELKNHWEELSKTYADROSR-----LKDCKQKQRYQ-2847
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 2894 RSLLEILNSAADILINSEADEDGRDBKAGINQMDAVTEBLQAKTOSLEMTORLREF-2953
 1102 KE-IKNFRKCSSTERSAPNLVSHPQTMWENNKKYIMGNVCA-----LTSOKTAKGYEK-1154
 2954 QESFKNI EK-KVEGA-----KHGLEIFDALG--SQACSNKLEKIRAOQEVLOALIEP-3002
 1155 KPQKIEN-PENLIMBEAN-----KKPKRPOYQYTMVKLDENSGTSPTTQOASGDN-1204
 3003 QVDYLRNFTQGLVEDADPDGSDASQLLHQAEVAQOEFLEVKRQVNSG--VMKEN-3054
 1205 TPTTLTHPVAKPTFRWFEWGESFCERKRYLKOIKVDCYEN-GDVGRCSG-----1256
 3055 K-----LEGIGQFHCVRHEMFSQLADLDBDGMGAIGRDTSLQ901E-3098
 1257 -----DGEACDSISTHDYSTVSPNCPG-----CGKHCSSYRKWERKK-1295
 3099 DVRLFLNKIHVILKLDIEASEACRHMLEEGBETLIDLGLKRELBALNKQCG--KLTGRGX-3155
 1296 IEFHKQSAVQOQTDAIRNNNGNTPDKEFCITLETWPAAFRLKNGPKCTKKEVGD-1355
 3156 AR-----QEOLELTIGVEDFYRKU-KGLNDATTAAEBEAL--OMVGT-3197
 1356 DIDFEK-----DSKTFQHTCYGCPCKFKTNGONG-----NCGVSGILNGCDDGX-1400
 3198 EVELIINOGLADPKMFO-KEQYDPL-QMGLQOVNGLGGLISAGKDCDVOGLBH-----3249
 1401 SIDAKEI-AKMRSSITDVVMEVSDNDNTFEGDDIKDACHANIPKGIKQV--WKGYV-1457
 3250 --DMEIYARWNTLTKKVAQRIIA-----QLOEALHLCKGRFODALEPLLSWLD--3295
 1458 CGVDICEGQTNINERTDGEYEQIRALF--KAWVENFLEDYKINDKISHCIKKGSGSCI-1515
 3296 -----TEELIANQKPPSAEYKVAQIOEKLOLRLDDRAKYDML--QAQSGIYA-3345
 1516 NGCEKNSKCLKMEKKAIAEMENIKGRFND-----QYENKQDPDY-1555
 3346 QSAEILADR-----EKITGOLESLESKRTTELSKRAAOKOLEDLVLAKQPHETAEPLIS-3399
 1556 NVKSLIELEILPKIAVNDQDNVILKLVENSNGKCTLLISNTONKENDAIID-1605
 3400 DFLSTVEKKLANSEPVGTQAKIQOQIRHKA-----LEBDINHAHTD-3442

Search completed: December 29, 2005, 23:40:20
 Job time : 32.2054 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 23:10:51 ; Search time 9.4698 Seconds
(without alignment)

3623.140 Million cell updates/sec

Title: US-09-508-967-1_COPY_1_415

Perfect score: 2276

Sequence: 1 MATSGSGSGGQDDEDAKHYLD.....GSYENWIDNQRKQPKQKKY 415

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1010	44.4	2182	1	US-08-487-826B-16
2	956	42.0	2710	1	US-08-568-459A-12
3	956	42.0	2710	1	US-08-487-826B-12
4	956	42.0	2710	2	US-09-210-288-12
5	956	42.0	2710	2	US-10-153-273-12
6	956	42.0	3060	1	US-08-487-826B-14
7	845	37.1	700	1	US-08-568-459A-10
8	845	37.1	700	1	US-08-487-826B-10
9	845	37.1	700	2	US-09-210-288-10
10	845	37.1	700	2	US-10-153-273-10
11	690	30.3	3542	2	US-10-087-013-2
12	379.5	16.7	362	1	US-08-568-459A-18
13	379.5	16.7	362	1	US-08-487-826B-18
14	379.5	16.7	362	2	US-09-210-288-18
15	379.5	16.7	362	2	US-10-153-273-18
16	360.5	15.8	411	1	US-08-568-459A-19
17	360.5	15.8	411	1	US-08-487-826B-19
18	360.5	15.8	411	1	US-09-210-288-19
19	360.5	15.8	411	2	US-10-153-273-19
20	304	13.4	1435	1	US-08-568-459A-4
21	304	13.4	1435	1	US-08-487-826B-4
22	304	13.4	1435	2	US-09-210-288-4
23	304	13.4	1435	2	US-10-153-273-4
24	285.5	12.5	749	1	US-08-568-459A-6
25	285.5	12.5	749	1	US-08-487-826B-6
26	285.5	12.5	749	2	US-09-210-288-6
27	285.5	12.5	749	2	US-10-153-273-6

28	241	10.6	921	1	US-08-568-459A-8	Sequence 8, Appli
29	241	10.6	921	1	US-08-487-826B-8	Sequence 8, Appli
30	241	10.6	921	2	US-09-210-288-8	Sequence 8, Appli
31	241	10.6	921	2	US-10-153-273-8	Sequence 8, Appli
32	239	10.5	1115	1	US-08-568-459A-2	Sequence 2, Appli
33	239	10.5	1115	1	US-08-487-826B-2	Sequence 2, Appli
34	239	10.5	1115	2	US-09-210-288-2	Sequence 2, Appli
35	239	10.5	1115	2	US-10-153-273-2	Sequence 2, Appli
36	239	10.5	1115	6	5198347-6	Patent No. 5198347
37	233	10.2	407	2	US-10-087-013-8	Sequence 8, Appli
38	229.5	10.1	311	2	US-10-087-013-10	Sequence 10, Appli
39	218	9.6	308	2	US-10-087-013-11	Sequence 11, Appli
40	216.5	9.5	351	2	US-10-087-013-9	Sequence 9, Appli
41	207	9.1	294	2	US-10-087-013-7	Sequence 7, Appli
42	197.5	8.7	411	1	US-08-568-459A-20	Sequence 20, Appli
43	197.5	8.7	411	1	US-08-487-826B-32	Sequence 32, Appli
44	197.5	8.7	411	2	US-09-210-288-20	Sequence 20, Appli
45	197.5	8.7	411	2	US-10-153-273-20	Sequence 20, Appli

ALIGNMENTS

RESULT 1
US-08-487-826B-16
Sequence 16, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487, 826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29, 655
REFERENCE/DOCKET NUMBER: NIH121, 001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2182 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-487-826B-16
Query Match 44.4%, Score 1010, DB 1, Length 2182;

[illegible]

RESULT 2
 US-08-568-459A-12
 Sequence 12, Application US/08568459A
 Patent No. 5849306
 GENERAL INFORMATION:
 APPLICANT: Sim, Kim L.
 APPLICANT: Chienis, Cheran
 APPLICANT: Miller, Louis H.
 APPLICANT: Peterson, David S.
 APPLICANT: Su, Xin-zhaun
 APPLICANT: Wellems, Thomas E.
 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe Martens Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: US
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/568,459A
 FILING DATE: 07-DEC-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelsen, Ned
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: NIH121.001CPI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176

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; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 2710 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     HYPOTHEICAL: NO
;     ORIGINAL SOURCE:
;     ORGANISM: Plasmodium falciparum
; US-08-568-459A-12

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Query Match	42.0%	Score	956	DB	1	Length	2710
Best Local Similarity	46.4%	Pred.	No.	3.5e-77			
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							Gaps
							13
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QY	168	PGSDPFCMCTMLARSFADIGDIIRGRDYLGNKKKKONGKETEREKLEJOKLKEIFKIHND	227				
Db	179	GDSSQJCTMLARSFADIGDIVRDRDLYLGNPQIK-----QROGLENNIKTIFGKIYEK	233				
QY	228	LKDYEAKRINXGDEDPNPFYKLREDMWTANRETTWGAMTCSKELNDSYFRATCTNDTQGP	287				
Db	234	LNGAEA--RYG--NDPEFPKLREDMWTANRETTWKATTCANW--GNTYFHAHC--RG-	283				
QY	288	SQTNKKRCRCDKOGKANGKPKAGGADVIVTTFYEDVYPOYLRFMEEMADECRKKKKLLE	347				
Db	284	ERTKGYCRCDNDQ-----VTTYDDYPOYLRFMEEMADECRKKKKIK	327				
QY	348	NLEKQCKGKDSDEYRYCSRNGVCEOTISKKGKVRMGKGTDCFPACGSYENMIIDNQRK	407				
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QY	408	QEDKOKK	414				
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1      RESULT 3
2      US-08-487-826B-12
3      Sequence 12, Application US/08487826B
4      Patent No. 5993827
5      GENERAL INFORMATION:
6      APPLICANT: Sim, Kim L.
7      APPLICANT: Chitnis, Checan
8      APPLICANT: Miller, Louis H.
9      APPLICANT: Peterson, David S.
10     APPLICANT: Su, Xin-zhaun
11     APPLICANT: Weljems, Thomas E.
12     TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
13     TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING
14     NUMBER OF SEQUENCES: 45
15     CORRESPONDENCE ADDRESS:
16     ADDRESSEE: Knobbe Martens Olason & Bear
17     STREET: 620 Newport Center Drive 16th Floor
18     CITY: Newport Beach
19     STATE: California
20     COUNTRY: US
21     ZIP: 92660
22     COMPUTER READABLE FORM:
23     MEDIUM TYPE: Floppy disk
24     COMPUTER: IBM PC compatible

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01  OPERATING SYSTEM:  PC-DOS/MS-DOS
02  SOFTWARE:  Patent In Release #1.0, Version #1.2
03  CURRENT APPLICATION DATA:
04  APPLICATION NUMBER:  US/08/487,826B
05  FILING DATE:  10-SEP-1993
06  CLASSIFICATION:  435
07  ATTORNEY/AGENT INFORMATION:
08  NAME:  Israelien, Ned
09  REGISTRATION NUMBER:  29,655
10  REFERENCE/DOCKET NUMBER:  NIH21.001CPI
11  TELECOMMUNICATION INFORMATION:
12  TELEPHONE:  (619) 235-8550
13  TELEFAX:  (619) 235-0176
14  INFORMATION FOR SEQ ID NO: 12:
15  SEQUENCE CHARACTERISTICS:
16  LENGTH: 2710 amino acids
17  TYPE: amino acid
18  STRANDEDNESS: single
19  TOPOLOGY: linear
20  MOLECULE TYPE: protein
21  HYPOTHEetical: NO
22  ORIGINAL SOURCE:
23  ORGANISM: Plasmodium falciparum
24  JS-08-487-826B-12

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Query match 42.0%; Score 956; DB 1; Length 2710;

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Db      68 QTPEDPCDLHXKHTNVNTN-VINPCADRSVRFSDYEGGQCTHNRIKDSQGDNDKG---123
QY      108 SNGMTCAFPRRHLCKNKF PNNANSDS SIAKXHDLLAEVGMALYBESIKTHYFKYDSKY 167
Db      124 ----ACAYRRRLAVCDQNDQIEPIKITNT-NHLVADVCMAAAFESQISITQDPKYQATY 178
QY      168 PGSDPEMCTMLARSPADIGDIRGRDLYGNKKKKONGKETEREKLEOKLKEIFKKIHDN 227
Db      179 GDSPEQICTMLARSPADIGDIRGRDLYGNPQEIK-----QROQLNNLKTI FGKIY EK 233
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Db      234 LKGAEA--RYG--NDPEFPKLR EDWMTANRETVKKAITCNW--GNTYFATCN---RG- 283
QY      288 SQTNNKRCRDCKDKGANAAGKPKAGDGVTVI VPIYEDVVPOLRFEEMARDFCKKKKKKLE 347
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Db      388 QPDKQK 394

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RESULT 4
US-09-210-288-12
; Sequence 12, Application US/09210288

1 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 2 TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
 3 NUMBER OF SEQUENCES: 37
 4 CORRESPONDENCE ADDRESS:
 5 ADDRESSEE: Knobe Martens Olson & Bear
 6 STREET: 620 Newport Center Drive 16th Floor
 7 CITY: Newport Beach
 8 STATE: California
 9 COUNTRY: US
 10 ZIP: 92660
 11 COMPUTER READABLE FORM:
 12 MEDIUM TYPE: Floppy disk
 13 COMPUTER: IBM PC compatible
 14 OPERATING SYSTEM: PC-DOS/MS-DOS
 15 SOFTWARE: PatentIn Release #1.0, Version #1.25
 16 CURRENT APPLICATION DATA:
 17 APPLICATION NUMBER: US/09/210,288
 18 FILING DATE:
 19 CLASSIFICATION:
 20 ATTORNEY/AGENT INFORMATION:
 21 NAME: Fuller, Michael
 22 REGISTRATION NUMBER: 36,516
 23 REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
 24 TELECOMMUNICATION INFORMATION:
 25 TELEPHONE: (619) 235-6550
 26 TELEFAX: (619) 235-0176
 27 INFORMATION FOR SEQ ID NO: 12:
 28 SEQUENCE CHARACTERISTICS:
 29 LENGTH: 2710 amino acids
 30 TYPE: amino acid
 31 STRANDEDNESS: single
 32 TOPOLOGY: linear
 33 MOLECULE TYPE: protein
 34 HYPOTHEICAL: NO
 35 ORIGINAL SOURCE:
 36 ORGANISM: Plasmodium falciparum
 37 US-09-210-288-12

Query Match	42.0%;	Score 956;	DB 2;	Length 2710;
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[illegible]

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RESULT 5
US-10-153-273-12
; Sequence 12, Application US/10153273
; Patent No. 6962987
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; Chitnis, Chetan
; Miller, Louis H.
; Peterson, David S.
; Su, Xin-zhaun
; Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/153,273
APPLICATION DATA:
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FMV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-153-273-12

Query Match          42.0%; Score 956; DB 2; Length 2710;
Best Local Similarity 46.4%; Pred. No. 3,56-77;
Matches 198; Conservative 56; Mismatches 111; Indels 62; Gaps 13;

      4  SGSGCGTODEDAKVLDFGQKHDEYHGKAQNVSELKGSLSLAIAGTAFTVKSMQT 63
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db       14 AAGGDIDESAKMHFDRIQDVVDKYAEAKRKGKLQRLS-----EAKFEKNESP 67
Match    198; Conservative 56; Mismatches 111; Indels 62; Gaps 13;

      QY      64 ES-----KYTELLEANSKRPRCK-----KDGGNDVDVRFSVGEQAGDNKKMK 107
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Db       68 QTPEDPCDLDRKHTNTVTN--VINPQADRSVRSDEYGGQCTHNRIKDSQQGDNGK--- 123
Match    108 SNGMTCAEFRRLLHCNKNFPMNSNDSSKANGDILAEVCMAAKYGESIKTHVPKYSKY 167
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db       124 ----ACAPYRRHLHVCDQLBQIEPIKITNT--HNLLVDDVCAAKEFGGSIIDDPFKYQATY 178
Match    168 PGGDPFCQMLAARGADLDGIIRGRDLYLGNKKKKKKQNGKETEREKLEPKQKELFFKTIHDN 227
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Db      177 GDSBQICMLARSPADIGDIVRGHDLVLGNPQEIK-----QFOQLJENNLTITGIYK 233
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Db      234 LNGAEK--RYG--NDPEFFKLREDWWTANREIYWGALITCNAM--GNIFYPATCN--RG- 283
Qy      288 SOTHNRCRDCKGKAGNAGKPKAGDGVIVPTFYEDYVQYLRFWEEMAEADFCRKKKKLE 343
Db      284 ERTKGYCRGENDQ-----VPTFYDVYQYLRFWEEMAEADFCRKKKKIK 327
Qy      348 NLEKQCRGKDSDEIYRCNRNGYDCEQITSRKGRKRMKGGCTDCEPACGSIEMIIDQRK 407
Db      328 DVARNRGKDKEDKEDRYCSRNGYDCEKTKRAIGKLRYGKQICISCLYACNPYVDWINNQE 387
Qy      408 QPDKKK 414
Db      388 QPDKKK 394

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QY 64 ES-----KYTELLIANSKRNPK-----KDGKANDVDRSPVKEAGYDNKKMKC 107
DB 66 QTPEDPCOLDKHYNVTN-VINPCADRSVDRSPDEVGQCTNHRIDISQGNK--- 121
QY 108 SNGTCAPFRLHLCKNKPNNNSNDSSKAKHDLIAEVCMAKYEGESIKTHYPKYDSKY 167
DB 122 ----ACAPYRRLHVCDQMLEQLEPIKINT--HNLIVDCMAKFEQGSITODYPRYQATY 176
QY 168 PGSDPMTMLARSPADIGDIIRGRDLYLGNKKKKQKQKTEREKLKLEIFKKIDN 227
DB 177 GDSQITMTLARSPADIGDIVRGDLYLGNPQETK-----ORQLENNLKITIFKITYEK 231
QY 228 LKDKAQRKYNQDEDPNFYKJREDWMTANRETVMGAMTCSKELDSSYFRATCNDTGOGP 287
DB 232 LINGAE--RYG--NDPERFKLREDWMTANRETVMKALITCNAM--GNTYFHTCN---RG- 281
QY 288 SQTNNKCRDCKDKGNAGKPKAGDGVTVPTYPDYVPOYLRFPEWMAEDFCRKKKKYLE 347
DB 282 ERTKGVCRCNDQ-----VPTYFDYVPOYLRFPEWMAEDFCRKKKKIK 325
QY 348 NLEKQCRGKDSDEYRCSRNGYDCEOTISRKGKVRMGKCTDCEFFAGSYENMTIDNQRK 407
DB 326 DVKNCRCRQKDEKDRYCSRNGYDCEKTKRAIGKLRYGKQCTSLYACNPYVDWINNKE 385
QY 408 QFDKOKK 414
DB 386 QFDKOKK 392

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RESULT 7
US-08-568-459A-10
; Sequence 10, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,459A
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelien, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-0176
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 10:
; LENGTH: 700 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
US-08-568-459A-10

```

```

Query Match 37.1%; Score 845; DB 1; Length 700;
Best Local Similarity 54.9%; Pred. No. 6,2e-68;
Matches 168; Conservative 43; Mismatches 59; Indels 36; Gaps 10;

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QY 113 CAPFRLHLCKNKPNNNSNDSSKAKHDLIAEVCMAKYEGESIKTHYPKYDSKYPGDF 172
DB 10 CAPFRLHLCKY---NSESIDTSTYKLLLEVCMAYEENSINTHTOHOFTNEDSAS 66
QY 173 PMCTMLARSPADIGDIIRGRDLYLG--NKKKKQKQKTEREKLKLEIFKKIH-DWLK 229
DB 67 QCTVTLARSPADIGDIVRGDLYLGYDNKEQ-----RKLQKQKLDIKKIKHDKVMK 120
QY 230 DKAQKRYNGD-EDPNFYKJREDWMTANRETVMGAMTCSKELDSSYFRATCNDTGOGPS 288
DB 121 TNGAQERYIDAKAGDFPQJLRREDWMTSNRETVMKALICHAPKANYFIKTACN-VGKG-- 177
QY 289 QTNKCRDCKDKGNAGKPKAGDGVTVPTYPDYVPOYLRFPEWMAEDFCRKKKKYLEN 348
DB 178 -TNGQCHC-----IGGD-----VPTYFDYVPOYLRFPEWMAEDFCRKKKKYLEN 220
QY 349 LKQCRGKDSDEYRCSRNGYDCEOTISRKGKVRMGKCTDCEFFAGSYENMTIDNQRK 408
DB 221 LQKCRDYBQN---LYCSGNGYDCTKTYKKGKLVIGBHTNCSVCMETWTIDNQRK 277
QY 409 FDKOKK 414
DB 278 FLKOKR 283

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RESULT 8
US-08-487-826B-10
; Sequence 10, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelien, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-0176
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 10:
; LENGTH: 700 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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LENGTH: 700 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
US-08-487-8268-10

Query Match 37.1%; Score 845; DB 1; Length 700;
Best Local Similarity 54.9%; Pred. No. 6,2e-68;
Matches 168; Conservative 43; Mismatches 59; Indels 36; Gaps 10;

QY 113 CAPRRLHLCNKPFPNNNSNDSSKAKHDLAEVCAAKYEGESIKTHYPKYDSKYPGSDF 172
DB 10 CAPRRLHLCDY--NLESITSTTHKLLEVCMAKYEGNSINTHYTORNEBSAS 66
QY 173 PMCTMLARSPADIGDIIRGDLVYG--NKKKKQKETEREKLEOKLEIFKXIH-DNLK 229
DB 67 QLCVTLARSPADIGDIIRGDLVYGDKKEQ-----RKLEQKLDIFKXIHDKVMK 120
QY 230 DKAQRKRYND-EDPNFYKLREDMTANRETVGMATCSKELDNSSYFRATCNDTGGPS 288
DB 121 TNGAQRERYIDDAKAGDFQLRDMWTSNRETVGMALICHAPKEANYFIKTAQN-VGKG-- 177
QY 289 QTHNRCRCDDKDGKAGNAGKPGAGDGVTVPTYPFYVPOYLRFPEMAEDPFRKKKKKLEN 348
DB 178 -TNGQCHC-----IGD-----VPTYPFYVPOYLRFPEMAEDPFRKKKKKLEN 220
QY 349 LEKQCRGKSDERYVCSRGYDCQOTISRKGKVMGKGTDCFPFAGSYENWIDNORKQ 408
DB 221 LQKQCRDYEQN---LYCSGNGYDCTKTIYKKGKLVIGSHCTNCSVCMETWIDNORKQ 277
QY 409 FDKQKK 414
DB 278 FLQKQR 283

RESULT 9

US-09-210-288-10
Sequence 10, Application US/09210288
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb Martens Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
US-09-210-288-10

Query Match 37.1%; Score 845; DB 2; Length 700;
Best Local Similarity 54.9%; Pred. No. 6,2e-68;
Matches 168; Conservative 43; Mismatches 59; Indels 36; Gaps 10;

QY 113 CAPRRLHLCNKPFPNNNSNDSSKAKHDLAEVCAAKYEGESIKTHYPKYDSKYPGSDF 172
DB 10 CAPRRLHLCDY--NLESITSTTHKLLEVCMAKYEGNSINTHYTORNEBSAS 66
QY 173 PMCTMLARSPADIGDIIRGDLVYG--NKKKKQKETEREKLEOKLEIFKXIH-DNLK 229
DB 67 QLCVTLARSPADIGDIIRGDLVYGDKKEQ-----RKLEQKLDIFKXIHDKVMK 120
QY 230 DKAQRKRYND-EDPNFYKLREDMTANRETVGMATCSKELDNSSYFRATCNDTGGPS 288
DB 121 TNGAQRERYIDDAKAGDFQLRDMWTSNRETVGMALICHAPKEANYFIKTAQN-VGKG-- 177
QY 289 QTHNRCRCDDKDGKAGNAGKPGAGDGVTVPTYPFYVPOYLRFPEMAEDPFRKKKKKLEN 348
DB 178 -TNGQCHC-----IGD-----VPTYPFYVPOYLRFPEMAEDPFRKKKKKLEN 220
QY 349 LEKQCRGKSDERYVCSRGYDCQOTISRKGKVMGKGTDCFPFAGSYENWIDNORKQ 408
DB 221 LQKQCRDYEQN---LYCSGNGYDCTKTIYKKGKLVIGSHCTNCSVCMETWIDNORKQ 277
QY 409 FDKQKK 414
DB 278 FLQKQR 283

RESULT 10

US-10-153-273-10
Sequence 10, Application US/10153273
Patent No. 6962887
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb Martens Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-153-273-10

Query Match 37.1%; Score 845; DB 2; Length 700;
Best Local Similarity 54.9%; Pred. No. 6.2e-68;
Matches 168; Conservative 43; Mismatches 59; Indels 36; Gaps 10;

QY 113 CAPRRRLHLCNKNFPMNNSNDSSKAKHDLAEVCAAYEGESIKTHYPKYDSKYPGSDP 172
DB 10 CAPRRRLHLCY---NLESIDTSTTHKLLEVCMAAYEGNSINTHTYQRTNEDSAS 66
QY 173 PMCTMLARSPADIGDIIRGRDLYLGC--NKKKKQKQKTEREKKLEIKKIKH-DLK 229
DB 67 QLCVTLARSPADIGDIYRGDLYLGYDKKEQ-----RKLEQKDKIDFKKIHKDVWK 120
QY 230 DKEQKRNCGD-EDPNFYKLREDMWTANRETYWGAMTCSKELDNSYFRATCNDTGQSPS 288
DB 121 TNGQDERYIDAKGDPFQLREDMWTSNRETYWKALICHAKREANYPIKTACN-VGKG-- 177
QY 289 QTHNKRCDKDKGNAAGKPKAGDGVITVPTTFDYVPQYLRFEEWADFCRKKKKKLEN 348
DB 178 -TNGQCHC-----IGSD-----VPTTFDYVPQYLRFEEWADFCRKKKKKLEN 220
QY 349 LEKQCKGKSDERYCRNGYDCEQTSRKQKVRMGKCTDCFFACSGYENWIDNRQKQ 408
DB 221 LQKQCRDYEQN---LYSGNGYDCTKTIYKKGKLVIGHCTNCSYWCMTWETWIDNRKCE 277
QY 409 FDKQKK 414
DB 278 FLKQKR 283

RESULT 11
US-10-087-013-2
Sequence 2, Application US/10087013
Patent No. 6855323
GENERAL INFORMATION:
APPLICANT: Arthur Scherf
APPLICANT: Louis H. Miller
APPLICANT: Benoit Gamaun
APPLICANT: Dior I. Baruch
APPLICANT: Pierre Buffet
APPLICANT: Christine Scheidig
APPLICANT: Jurg Gysin
APPLICANT: Bruno Pavellie
APPLICANT: No. 685533Jufaka Fujii
APPLICANT: Joseph Smith
TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
TITLE OF INVENTION: (PFEMP1) THAT MEDIATES ADHESION TO CHONDROITIN SULFATE A
FILE REFERENCE: NIH176.001C1
CURRENT APPLICATION NUMBER: US/10/087,013

CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: PCT/US00/24195
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/152,023
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 3542
TYPE: PRT
ORGANISM: Plasmodium falciparum
US-10-087-013-2

Query Match 30.3%; Score 690; DB 2; Length 3542;
Best Local Similarity 38.3%; Pred. No. 7.3e-53;
Matches 162; Conservative 64; Mismatches 125; Indels 72; Gaps 19;

QY 13 EDAGHVLDFEQKV-HDEVHGEAKNYVSEKGISLASILIGETAFYTK----- 59
DB 33 KSAENVLERYAKNIRHPSKY--AKEHVDLSKGLDTKAEFRGSPSTPVAKHNYVYPCNL 90
QY 60 --SMQTSKYTELEANSKRNPCCKDGKNDVDFSVYEQAGYDNK---KQKSGNGWC 113
DB 91 DKHEHTMLRYDDV---NLRHPC---HGRQNRFDDEBESCGNKLRNYRK-NDATAC 141
QY 114 APPRRRLHLCNKNFPMNNSNDSSKAKHDLAEVCAAYEGESIKTHYPKYDSKYPGSDP 173
DB 142 APPRRRLHLCNKNFPMNNSNDSSKAKHDLAEVCAAYEGESIKTHYPKYDSKYPGSDP 173
QY 174 MCTMLARSPADIGDIIRGRDLYLGNKKKKQKQKTEREKKLEIKKIKH-DLK 233
DB 195 ACTALARSPADIGDIYRGDLYLGYDKKEQ-----KENVHDKVETGLREVFKKIHDKMED-EV 243
QY 234 QKRNGBEDPFFYKLREDMWTANRETYWGAMTCSKELDNSYFRATCNDTGQSPQSTNK 293
DB 244 KNDYNPDGSGNYTLRRAWMNVNKNWEALITCDASY-KSGYFMQESNT---PLFSNPK 299
QY 294 CRCQDKGNAAGKPKAGDGVITVPTTFDYVPQYLRFEEWADFCRKKKKKLENLEKQK 353
DB 300 C-----GHQKQ-----VPTTFDYVPQYLRFEEWADFCRKKKKKLENLEKQK 343
QY 354 RGKQSDERYCRNGYDCEQTSRKQKVRMGKCTDCFFACSGYENWIDNRQKQ 413
DB 344 R-NDK--ERLYCSNHGDCITTIWKGIHLDNKCTDCSTCKVFEWLGNGQEAFFKQK 400
QY 414 -KY 415
DB 401 EKY 403

RESULT 12
US-08-568-459A-18
Sequence 18, Application US/08568459A
Patent No. 5849306
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Willems, Thomas B.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Knodde Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459A
FILING DATE: 07-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelien, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-568-459A-18
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Query Match 16.7%; Score 379.5; DB 1; Length 362;

Best Local Similarity 31.3%; Pred. No. 4.6e-26; Matches 93; Conservative 14; Mismatches 149; Indels 41; Gaps 5;

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Oy 113 CAPRRRLHLCNKNFNNNSNDSSKAKHDLAEVCAATYEGESIKTHYPKYDSKYPGSDF 172
|||:|||||:|
2 CAPRRRLHLCY---NLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 58
Oy 173 PMSCTLARSPADIGDIRGRDLYIG--NKKKKQNGKTEREKLKELFKIHDNLKD 230
|||:|||||:|
Db 59 QLCIVLARSPADIGDIRGRDLYIGDNLKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 118
Oy 231 KEAQKRVNGDEDPNFKYLRREDMTANRETVGAMTCSKELDNSYFRATCNDTGGPSQT 290
|||:|||||:|
Db 119 XXXXXXXKGD---FQLRREDMTSNRETVKALICAXXXXXXXXXXXXXC----- 164
Oy 291 HNKCRCDKDGKAGNAGKPRAGDVTIVPTFYDVPQYLRFEEWAEDFCRKKKKLNTLE 350
|||:|||||:|
Db 165 -----XXXXXXXXXXXXXXXXXXXXXXXXXXVPQYLRFEEWAEDFCRKKKKLNTLQ 214
Oy 351 KQCRGKDSDEYRYCSRNGYDCEQITSRKGVKMGKCTDCCFPACGSEYEMIDNQRK 407
|||:|||||:|
Db 215 KQ-----CXKXXXXCXKXXXXXXXXXXXXXXXXXXCTNCSVCMYETWIDNQRK 259
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RESULT 13

US-08-487-826B-30
Sequence 30, Application US/08487826B
Patent No. 5993827

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelien, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-487-826B-30
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Query Match 16.7%; Score 379.5; DB 1; Length 362;

Best Local Similarity 31.3%; Pred. No. 4.6e-26; Matches 93; Conservative 14; Mismatches 149; Indels 41; Gaps 5;

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Oy 113 CAPRRRLHLCNKNFNNNSNDSSKAKHDLAEVCAATYEGESIKTHYPKYDSKYPGSDF 172
|||:|||||:|
2 CAPRRRLHLCY---NLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 58
Oy 173 PMSCTLARSPADIGDIRGRDLYIG--NKKKKQNGKTEREKLKELFKIHDNLKD 230
|||:|||||:|
Db 59 QLCIVLARSPADIGDIRGRDLYIGDNLKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 118
Oy 231 KEAQKRVNGDEDPNFKYLRREDMTANRETVGAMTCSKELDNSYFRATCNDTGGPSQT 290
|||:|||||:|
Db 119 XXXXXXXKGD---FQLRREDMTSNRETVKALICAXXXXXXXXXXXXXC----- 164
Oy 291 HNKCRCDKDGKAGNAGKPRAGDVTIVPTFYDVPQYLRFEEWAEDFCRKKKKLNTLE 350
|||:|||||:|
Db 165 -----XXXXXXXXXXXXXXXXXXXXXXXXXXVPQYLRFEEWAEDFCRKKKKLNTLQ 214
Oy 351 KQCRGKDSDEYRYCSRNGYDCEQITSRKGVKMGKCTDCCFPACGSEYEMIDNQRK 407
|||:|||||:|
Db 215 KQ-----CXKXXXXCXKXXXXXXXXXXXXXXXXXXCTNCSVCMYETWIDNQRK 259
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RESULT 14

US-09-210-288-18
Sequence 18, Application US/09210288
Patent No. 6392026

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California

```

1      COUNTRY: US
2      ZIP: 92660
3
4      COMPUTER READABLE FORM:
5      MEDIUM TYPE: Floppy disk
6      COMPUTER: IBM PC compatible
7      OPERATING SYSTEM: PC-DOS/MS-DOS
8      SOFTWARE: Patent Release #1.0, Version #1.25
9      CURRENT APPLICATION DATA:
10     APPLICATION NUMBER: US/09/210,288
11
12     FILING DATE:
13
14     CLASSIFICATION:
15
16     ATTORNEY/AGENT INFORMATION:
17     NAME: Fuller, Michael
18     REGISTRATION NUMBER: 36,516
19     REFERENCE/DOCKET NUMBER: NIH21,1FWDV1
20     TELECOMMUNICATION INFORMATION:
21     TELEPHONE: (619) 235-8550
22     TELEFAX: (619) 235-0176
23
24     INFORMATION FOR SEQ ID NO: 18:
25     SEQUENCE CHARACTERISTICS:
26     LENGTH: 362 amino acids
27     TYPE: amino acid
28     STRANDEDNESS: single
29     TOPOLOGY: linear
30     MOLECULE TYPE: peptide
31     HYPOTHETICAL: NO
32     ANTI-SENSE: NO
33     FRAGMENT TYPE: internal
34
35     ORIGINAL SOURCE:
36
37     US-09-210-288-18

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Query Match 16.7%; Score 379.5; DB 2; Length 362;
 Best Local Similarity 31.3%; Pred. No. 4.6e-26;
 Matches 93; Conservative 14; Mismatches 19; Indels 41; Gaps 5

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Qy 113 CAPFRLHLCNNQFNPNSSNDSSKAGHDLLAEVCMAKYESES1KTHPYKSDSKYFGSDP 172
Db 2 CAPYRRLHLCY---NLAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 58
Qy 173 PWCMTLASFADIGDIIRGRDLYLG--NKKKKONGETEREKLEQKLKE1FKKHIDNLKD 230
Db 59 QLCITLASFADIGDIIRGRDLYLGDNKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 118
Qy 231 KEAQGRNVGDEDPNYPYKLEDEDMWTANRETVMGAMTCSKELDSSVPYATCNDTPGQSPQT 290
Db 119 XXXXXXXXKGD---FFQLREDMWTSIRKETVMYKALITHAXXXXXXXXXXXXXXC----- 164
Qy 291 HNKCRCXDKDKGANNAKPKAGDGDVITVPYFDVYPOYLWFEEMWADFCRKKKKKLEMLE 350
Db 165 -----XXXXXXXXXXXXXXXXXXXXXXXXXXXXXVPYLWFEEMWADFCRKKKKKLEMLQ 214
Qy 351 KQCRGKSDSEVRYSRNGYDCEQRTSRKGYRVMGSGCJDCFFACGSYEWIMIDNOKR 407
Db 215 KQ-----CXXXXXXCXXXXXXXXXXXXXXXXXXXXCTNCSYVWCWMEYETEMIDNOKR 259

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RESULT 15
US-10-153-273-18
Sequence 18, Application US/10153273
Patent No. 6962987
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
Chicnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach
 STATE: California
 COUNTRY: US
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/153,273
 FILING DATE: 21-May-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/210,268
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Fuller, Michael
 REGISTRATION NUMBER: 36,516
 REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 362 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Query Match	16.7%;	Score 379.5;	DB 2;	Length 362;
Best Local Similarity	31.3%;	Pred. No. 4.6e-26;		
Matches	93;	Conservative	14;	Mismatches 149;
			Indels	41;
			Gaps	5.

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Search completed: December 29, 2005, 23:17:19
Job time : 11.4698 secs

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OM protein - protein search, using sw model1

Run on: December 29, 2005, 23:15:07 ; Search time 45.2601 Seconds
(without alignments)
3831.174 Million cell updates/sec

Title: US-09-508-967-1_COPY_1_415
Perfect score: 2276
Sequence: 1 MATSGSGSGGTDEDAKHVLD.....GSYENWIDNOKRQFKQKKY 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	956	42.0	2710	US-10-153-273-12	Sequence 12, Appl
2	845	37.1	700	US-10-153-273-10	Sequence 10, Appl
3	690	30.3	3542	US-10-087-013-2	Sequence 2, Appl
4	379.5	16.7	362	US-10-153-273-18	Sequence 18, Appl
5	360.5	15.8	411	US-10-153-273-19	Sequence 19, Appl
6	318	14.0	1143	US-09-924-154-14	Sequence 14, Appl
7	318	14.0	1210	US-10-677-980-2	Sequence 2, Appl
8	304	13.4	1435	US-10-153-273-4	Sequence 4, Appl
9	293	12.9	616	US-10-293-913A-4	Sequence 4, Appl
10	292	12.8	616	US-10-293-913A-2	Sequence 2, Appl
11	292	12.8	1421	US-09-924-154-13	Sequence 13, Appl
12	285.5	12.5	749	US-10-153-273-6	Sequence 6, Appl
13	285.5	12.5	1086	US-09-924-154-15	Sequence 15, Appl
14	241	10.6	921	US-10-153-273-8	Sequence 8, Appl
15	239	10.5	1115	US-10-153-273-2	Sequence 2, Appl
16	238	10.5	972	US-09-924-154-16	Sequence 16, Appl
17	233	10.2	407	US-10-087-013-8	Sequence 8, Appl
18	229.5	10.1	311	US-10-087-013-10	Sequence 10, Appl
19	218	9.6	308	US-10-087-013-11	Sequence 11, Appl
20	216.5	9.5	351	US-10-087-013-9	Sequence 9, Appl
21	216.5	9.5	1501	US-09-924-154-17	Sequence 17, Appl
22	216.5	9.5	1568	US-10-712-533A-12	Sequence 12, Appl
23	207	9.1	294	US-10-087-013-7	Sequence 7, Appl
24	197.5	8.7	411	US-10-153-273-20	Sequence 20, Appl
25	159.5	7.0	282	US-10-153-273-16	Sequence 16, Appl
26	158.5	7.0	277	US-10-153-273-15	Sequence 15, Appl
27	130.5	5.7	448	US-10-153-668-370	Sequence 370, App

28	126	5.5	291	4	US-10-153-273-13	Sequence 13, Appl
29	125.5	5.5	6761	5	US-10-732-923-15035	Sequence 15035, A
30	124	5.4	706	4	US-10-104-047-3843	Sequence 21, Appl
31	121	5.3	311	4	US-10-153-273-21	Sequence 254, App
32	119.5	5.3	754	5	US-10-153-668-254	Sequence 40642, A
33	118	5.2	737	5	US-10-450-763-40642	Sequence 30936, A
34	117	5.1	680	6	US-11-097-143-30936	Sequence 1486, Ap
35	116.5	5.1	1255	5	US-10-471-934-4	Sequence 145507, A
36	116.5	5.1	1257	4	US-10-408-765A-1486	Sequence 125002, A
37	115.5	5.1	281	4	US-10-424-599-145507	Sequence 152106, A
38	115.5	5.1	463	4	US-10-425-115-225002	Sequence 17, Appl
39	115.5	5.1	905	4	US-10-437-963-152106	Sequence 212, App
40	115	5.1	324	4	US-10-153-273-17	Sequence 107, App
41	114.5	5.0	610	3	US-09-989-920-212	Sequence 3351, Ap
42	114.5	5.0	665	3	US-09-820-843A-107	Sequence 194264, A
43	113	5.0	1985	5	US-10-732-923-3351	Sequence 35, Appl
44	112.5	4.9	1737	4	US-10-437-963-194264	
45	111.5	4.9	454	6	US-11-004-418A-35	

ALIGNMENTS

RESULT 1
US-10-153-273-12
; Sequence 12, Application US/10153273
; Publication No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
Childs, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbhe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum

SEQUENCE DESCRIPTION: SEQ ID NO: 12;
US-10-153-273-12

Query Match 42.0%; Score 956; DB 4; Length 2710;
Best Local Similarity 46.4%; Pred. No. 5.5e-71;
Matches 198; Conservative 56; Mismatches 111; Indels 62; Gaps 13;

4 SGSGGCTDEDAKHYLDFGQKVDHVEHGAKNYSELKSLASLIGETAFYVKSMT 63
14 AAGGDDIEDSAKMFRIKGVYDKVEAKERKGLQRLS-----EAKFEKNESDP 67
64 ES-----KYTELIANSKRNPK-----KDGKNDVDRSVKEQAGYNKKMKC 107
68 QTPEDPCDLKHVHTNVTN--VINFCARSDVRFESDEYGGQCTHNRIDSQGGNKG--- 123
108 SNGMTCAFERLHCNKNFPMNNSDSKAKHDLAEVCAAKYGESIKTHYPRKYSKY 167
124 ---ACAPYRLHVDQMLEQIBPIKINT--HNLVVDVCAAKYEGQSTQDYPRYQNTY 178
168 PGSDPMTMLARSPADIGDIIRGRDLYLGNKKKKKONGKETEREKLEQKLEIFKIH 227
179 GDSPEQICTMLARSPADIGDIIRGRDLYLGNPKIK-----QROLENNLKITIKIYK 233
228 LKDEAQRKRYNGDEDPNFYKLRDWMWTANRETWGMATCSKELDSSYFRATCNDTGGP 287
234 LAGABA--RYG--NDPEFKLRDWMWTANRETWGMATCSKELDSSYFRATCNDTGGP 283
268 SOTHNKCRCDKXGNAKPKRAGDGVTVIPYFPYVQYLRWFEEMADEFCRKKKKLE 347
284 ERTKGYCRCDNDQ-----VPTFPYVQYLRWFEEMADEFCRKKKKIK 327
348 NLEKCRGKDSDEYRYSRNGYDCEQITSRKGYRWMKGGCTDCEPAGSYENWIDNORK 407
368 DVKRCRCKDKEDKORYCSRNGYDCEKTKRAIKGLRYKQKQICSLYACNPYDWINNKE 387
408 QFDKOKK 414
388 QFDKOKK 394

RESULT 2
US-10-153-273-10
Sequence 10, Application US/10153273
Publication No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knodde Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-153-273-10

Query Match 37.1%; Score 845; DB 4; Length 700;
Best Local Similarity 54.9%; Pred. No. 2.3e-62;
Matches 168; Conservative 43; Mismatches 59; Indels 36; Gaps 10;

113 CAPFRHLHCNKNFPMNNSDSKAKHDLAEVCAAKYGESIKTHYPRKYSKYPSDF 172
10 CAPFRHLHCNKNFPMNNSDSKAKHDLAEVCAAKYGESIKTHYPRKYSKYPSDF 172
173 PMCTMLARSPADIGDIIRGRDLYLGNKKKKKONGKETEREKLEQKLEIFKIH-DNLK 229
67 QLTVALRSPADIGDIIRGRDLYLGNPKIK-----RKDLQKLDIFKIKHDKVMK 120
230 DKEAQRKRYNGDEDPNFYKLRDWMWTANRETWGMATCSKELDSSYFRATCNDTGGPS 288
121 TNGQERYIDAKAGDFQRLREDWMTSNRETWGMATCSKELDSSYFRATCNDTGGPS 177
289 QTNHCRCDKXGNAKPKRAGDGVTVIPYFPYVQYLRWFEEMADEFCRKKKKLEN 348
178 -TNGQCHC-----TNGD-----VPTFPYVQYLRWFEEMADEFCRKKKKLEN 220
349 LEKCRGKDSDEYRYSRNGYDCEQITSRKGYRWMKGGCTDCEPAGSYENWIDNORK 408
221 LQKCRDYEON--LYCSGNGYDCEKTKRAIKGLRYKQKQICSLYACNPYDWINNKE 277
409 FDKOKK 414
278 FDKOKK 283

RESULT 3
US-10-087-013-2
Sequence 2, Application US/10087013
Publication No. US20040062769A1
GENERAL INFORMATION:
APPLICANT: Arthur Scherf
APPLICANT: Louis H. Miller
APPLICANT: Benoit Gamain
APPLICANT: Dior I. Baruch
APPLICANT: Pierre Buffet
APPLICANT: Christine Scheidig
APPLICANT: Jurg Gysin
APPLICANT: Bruno Pouvelle
APPLICANT: No. US20040062769A1utaka Fujii
TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
FILE REFERENCE: NIH176.001C1
CURRENT APPLICATION NUMBER: US/10/087, 013
FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: PCT/US00/24195
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/152,023

PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 3542
TYPE: PRT
ORGANISM: Plasmodium falciparum
US-10-087-013-2

Query Match 30.3%; Score 690; DB 4; Length 3542;
Best Local Similarity 38.3%; Pred. No. 2.3e-48;
Matches 162; Conservative 64; Mismatches 125; Indels 72; Gaps 19;

QY 13 EDAAKVLDFEFGKV-HDEVHGAQKYYVEISLGLSLAIIIGTATYK-----59
DB 33 KSARVTLRYAKNIHPSKY-AKEHVSLKGLDYLKAEFRGGPSIPVKNHNYTPPCNL 90
QY 60 --SMQESKYTELIRANSKRNPKCKDKGNDVDFPSVEQAGYDNK---KMKCSNGMTC 113
DB 91 DHKHTNLRYDDV---NLRHPC---HGREQNRDEDESECGKINRYRK-NDALAC 141
QY 114 APERRLHLCNKNFPMNSNDSSKAGHDLAEVCMARYEGESIKTHYPKDYSGSDFP 173
DB 142 APPRRRHMCNKLKALNDINTQNI-HDLIGNVLTAKYEGESIVNNHP-----HKGTG-D 194
QY 174 MCTMLARSPADIGDIIRGRDLYLGKNGKKKQNGKTEREKLBOQLKEIFKJHDNLKDEA 233
DB 195 ACTALARSFADIGDILVRGIDMF-----KPVNHDKVETGLAEVPRKJHDGKED-EV 243
QY 234 QKRYNGDDPNFYKLRBDWMTANRETVGAMTCSKELNDSYFRATCNDTGQSPGOTHNK 293
DB 244 KNDYVDPDSSGNYIKLREAMWNNRKNKWEATICDASY-KSGYFMGSEST---PLFSNPK 299
QY 294 CRCDKCANAGKPRAGDGVTVPTFYDYVPQYLRFWEVMAEDFCRKKKKLLENLEKQC 353
DB 300 C-----GHKQK-----VPTNLDYVQYLRFWEVMAEDFCRKKKILKQKVCOSC 343
QY 354 RKGKSDRYRCSRNGYDCEQOTISRKGKVRMGKCTDCEFPAGCSYENMIDNRKQFQK 413
DB 344 R-NDK--RRLYCSHNGHDCCTTIIWKGIHLHNKCTDCSTYCKVPEVWLNQDEAFKQK 400
QY 414 -KY 415
DB 401 EKY 403

RESULT 4

US-10-153-273-18
Sequence 18, Application US/10153273
Publication No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.

Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
Wellens, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Puller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-153-273-18
Query Match 16.7%; Score 379.5; DB 4; Length 362;
Best Local Similarity 31.3%; Pred. No. 2.1e-23;
Matches 93; Conservative 14; Mismatches 149; Indels 41; Gaps 5;

QY 113 CAPRRRLHLCNKNFPMNSNDSSKAGHDLAEVCMARYEGESIKTHYPKDYSGSDF 172
DB 2 CAPRRRLHLCY---NLKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 58
QY 173 PMCTMLARSPADIGDIIRGRDLYLG--NKKKQNGKTEREKLBOQLKEIFKJHDNLKD 230
DB 59 QLCYTLARSPADIGDIYAGKDLVGYDNKXXXXXXXXXXXXXXXXXXXXXXXXXXXX 118
QY 231 KEAQRYNGDDPNFYKLRBDWMTANRETVGAMTCSKELNDSYFRATCNDTGQSPGOT 290
DB 119 XXXXXXXKGD---FFQLREBDWMTSNRETWKALICHXXXXXXXXXXXXX----- 164
QY 291 HMKCRDCKANAGKPRAGDGVTVPTFYDYVPQYLRFWEVMAEDFCRKKKKLLENLEK 350
DB 165 -----XXXXXXXXXXXXXXXXXXXXXXXXXXXXVQYLRFWEVMAEDFCRKKKKLLENLEK 214
QY 351 KQCRGKSDRYRCSRNGYDCEQOTISRKGKVRMGKCTDCEFPAGCSYENMIDNRK 407
DB 215 KQ-----CXKXXXXXXXXXXXXXXXXXXXXCTNCSVCMRYETWIDNQK 259

RESULT 5

US-10-153-273-19
Sequence 19, Application US/10153273
Publication No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.

Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
Wellens, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660

```

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153.273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210.288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36, 516
REFERENCE/DOCKET NUMBER: NIH121.1FMDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-153-273-19

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Query Match      15.8%; Score 360.5; DB 4; Length 411;
Best Local Similarity 29.1%; Pred. No. 9.8e-22;
Matches 86; Conservative 22; Mismatches 155; Indels 33; Gaps 5;

QY 113 CAFPRRLHCNKNFPMNSNDSSKAKHDLAEVCAAYEGESIKTHYPKYDSKXPGSDF 172
DB 34 CAPYRLHVCQGNL-XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 92
QY 173 PQCMTLASFADIGIITIGRDLYLGNKKKKKNGKTEBEKLEQKLEIFKIHNLKKE 232
DB 93 QICTMLASFADIGIIVGRDYLGNPQEXXXXXX-----XXXXXXXXXXXXXXXXXX 143
QY 223 AQKRVNGEDPWFYTLREDMTANRETYGAWTCSKELDNSYFRATCNDTGGPSQTHN 292
DB 144 XXXXXXXXXXXXNDEFFKLRDMMTANRETYGAWTCSKELDNSYFRATCNDTGGPSQTHN 189
QY 293 KCRCDKAGNAGKPKAGDGVTVIPYFDYVPOYLRFEEWAEADFCRKKKKLENLKQ 352
DB 190 -----XXXXXXXXXXXXXXXXXXXXXXXXXXVPQYLRFEEWAEADFCRKKKKLENLKQ 241
QY 353 C-RGKQKDEYRYCSRNGYDCQGISRKGVKVMGKCTDCEFPACSYENMTDNQK 407
DB 242 CXXXXXXXXXXXXXCCCCXXXXXXXXXXXXXXXXXXXXCISCIYACNPYDWINQRE 297

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RESULT 6
US-09-924-154-14
Sequence 14, Application US/09924154
Patent No. US20020127241A1
GENERAL INFORMATION:
APPLICANT: Namum, David L.
APPLICANT: Sim, Kim L.
TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use
FILE REFERENCE: 05213-0465 43170-262105
CURRENT APPLICATION NUMBER: US/09/924.154
CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 60/223.525
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patent in version 3.1

```

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; SEQ ID NO 14
; LENGTH: 1143
; TYPE: PRT
; ORGANISM: Mammalian
US-09-924-154-14

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```

Query Match      14.0%; Score 318; DB 3; Length 1143;
Best Local Similarity 25.3%; Pred. No. 1.4e-17;
Matches 94; Conservative 53; Mismatches 97; Indels 128; Gaps 17;

QY 64 ESKYTELEANSKRNPKCKGKGNVD---RFSYKQAGY-----DNKKKCSNGM-- 111
DB 426 DCRITATITISFLNGPAK-----NDVDIASQINVDLRGCGNYSNNKSMCTGFTN 480
QY 112 ----TCAPFRRLHCNKNFPMNSNDSSKAKHDLAEVCAAYEGESIKTHYPKYDSKY 167
DB 481 KPPTCEPPRRQTLCLGRYTLRHGHBEDEYKHLG---ASIEAQLLKYKYEKEN- 535
QY 168 PGSDPQCMTLASFADIGIITIGRDLYLGNKKKKKNGKTEBEKLEQKLEIFKIHNL 227
DB 536 ----ALCSIIQNSYADLADIKSDII-----KQYGGKMEENLNKVK---DK 577
QY 228 LKQKQAKRYNGEDPWFYTLREDMTANRETYGAWTCSKELDNSYFRATCNDTGGP 287
DB 578 KRNESLKIF-----REKMDENKENYKVM--SAVLKN---KETCK----- 614
QY 288 SQTHNCRCDKAGNAGKPKAGDGVTVIPYFDYVPOYLRFEEWAEADFCRKKKKL- 346
DB 615 -----DYDK-----FQKLPQFLRFKMGWDCEFRKREKXY 645
QY 347 --ENLEKQCKGKDSERYCSRNGYDCQGISRKGVKMGKCTDCEFPACSYENMTDN 404
DB 646 SFESFPKVECKCKD-----CDEN-----TKNKKSEYKKWIDL 677
QY 405 ORKQEDKO-KKY 415
DB 678 KKSSEYKQVDKY 689

```

```

RESULT 7
US-10-677-980-2
Sequence 2, Application US/10677980
Publication No. US20050239730A1
GENERAL INFORMATION:
APPLICANT: Mayer, D.C.Gislaine
APPLICANT: Miller, Louis H.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE
FILE REFERENCE: NIH209.001C1
CURRENT APPLICATION NUMBER: US/10/677.980
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: PCT/US02/10071
PRIOR FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/281130
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1210
TYPE: PRT
ORGANISM: Plasmodium falciparum
US-10-677-980-2

```

```

Query Match      14.0%; Score 318; DB 5; Length 1210;
Best Local Similarity 25.3%; Pred. No. 1.6e-17;
Matches 94; Conservative 53; Mismatches 97; Indels 128; Gaps 17;

QY 64 ESKYTELEANSKRNPKCKGKGNVD---RFSYKQAGY-----DNKKKCSNGM-- 111
DB 420 DCRITATITISFLNGPAK-----NDVDIASQINVDLRGCGNYSNNKSMCTGFTN 474
QY 112 ----TCAPFRRLHCNKNFPMNSNDSSKAKHDLAEVCAAYEGESIKTHYPKYDSKY 167

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Db      475 KPGCTCEPRRQRLCLGRTYLLHGHGEEDYKHEHLG---ASITYEAOULLKYYKXKEDN- 529
Qy      168 PGSPFPMCTMLARSPADIGDIIIRGRDLVGNKKKKKQNGKETEREXLEJOKLKEIFPKXIHND 227
Db      530 -----ALCSTIIQNSTADLADIIKGSDII-----KDYKGGKMEENLKNVKN---DK 571
Qy      228 LKDKBAQKRYNGDEDPNFYKLRBEDWWTANRETVGAMTCSKELDNSSYFRATCNDTGGP 287
Db      572 KRNESESLKIF-----REKWMDEKNENVMKVM---SAVLKN-----KETCK----- 608
Qy      288 SQTNNKRCDDXKGNAGKPYAGDGVTVIPTYFDYVQYLRWPEEMADFCRKKKKL- 346
Db      609 -----DYDK-----FOKIPQFLRWFEKMGDDDFCEKRXKEXIY 639
Qy      347 --ENLEKQCRKXDSDEYRCSRGYDCEQTIISRKGRKMGKGTDCPFAGSYENMTDN 404
Db      640 SFESFKEVCKKKD-----CDEN-----TCNNKSEYKRWIDL 671
Qy      405 QRKQFDKQ-KKY 415
Db      672 KKSEYKQVDKY 683

```

```

RESULT 8
US-10-153-273-4
; Sequence 4, Application US/10153273
; Publication No. US20020169305A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
;             Chitnis, Chetan
;             Miller, Louis H.
;             Peterson, David S.
;             Su, Xin-zhaun
;             Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,273
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum

```

```

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-153-273-4

```

```

Query Match      13.4%; Score 304; DB 4; Length 1435;
Best Local Similarity 23.7%; Pred. No. 2,9e-16;
Matches 98; Conservative 55; Mismatches 124; Indels 136; Gaps 16;

```

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Qy      24 QKVHDEVHGEAKNY---VSELKGSLSASIIIGETAFYKSNQTE-SKY-----TELIEA 73
Db      387 QKVPEK---NAENYLIKISEKNDKAKVSLI-----NNDAYSKXCDCDKHTTLTVKS 436
Qy      74 --NSKNPCKKDGKANDVDRFSV---KEQAGYNNKKKCSNGM-----TCAPPRRIHL 121
Db      437 VLANGNDNTIKERKHIDLDPSFKGCDKNSVDVTWKMECNPYILSTKDVCPVPRREL 496
Qy      122 CNKQFPMNNSDSSKAGHDLLAEVCMAYGESIKTHHYRYSKPSQSPMCTMLARS 181
Db      497 CLGNIDRIYDKNLMIMEHLA-----IAIYESRLKRYKNDK-----EVCKIINKT 546
Qy      182 PADIGDIIIRGRDLVGNKKKKKQNGKETEREXLEJOKLKEIFPKXIHNDLKDEAQRKYNDE 241
Db      547 PADIRDIIGTDYV-----NDLSNRKLVGKINTNSKYVRANKNDKL----- 588
Qy      242 DPNFYKLRBEDWWTANRETVGAMTCSKELDNSSYFRATCNDTGGPSEQTHNKCDCXDKG 301
Db      589 -----FRDEWKKVYKKQVNVLI-----SWVFK-----DKTVCKEDDI 620
Qy      302 ANAGKPYAGDGVTVIPTYFDYVQYLRWPEEMADFCRKKKKLLENLEKQCRKXDSDE 361
Db      621 EN-----IPQFPRWFEWGDYCODTKRMILETLKYCEKKEPCEDD 660
Qy      362 YRCSRGYDCEQTIISRKGRKMGKGTDCPFAGSYENMTDNRKQFDKQK 414
Db      661 -----NCKSKNSYKEMISKKEEYNNQAK 685

```

```

RESULT 9
US-10-293-913A-4
; Sequence 4, Application US/10293913A
; Publication No. US20040022805A1
; GENERAL INFORMATION:
; APPLICANT: Natum, David
; APPLICANT: Liang, Hong
; APPLICANT: Fuhrmann, Steve
; APPLICANT: Sim, B. Kim Lee
; TITLE OF INVENTION: Synthetic Genes for Malarial Proteins and Methods of Use
; FILE REFERENCE: 05213-0464 (43170-280206)
; CURRENT APPLICATION NUMBER: US/10/293,913A
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/345,051
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic BBA-175 RII
US-10-293-913A-4

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```

Query Match      12.9%; Score 293; DB 4; Length 616;
Best Local Similarity 23.8%; Pred. No. 8.4e-16;
Matches 99; Conservative 54; Mismatches 121; Indels 142; Gaps 17;

```

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Qy      24 QKVHDEVHGEAKNY---VSELKGSLSASIIIGETAFYKSNQTE-SKY-----TELIEA 73
Db      243 QKVPEK---NAENYLIKISEKNDKAKVSLI-----NNDAYSKXCDCDKHTTLTVKS 292
Qy      74 --NSKNPCKKDGKANDVDRFSVKEQAGYD-----NKKKKCSNGTCAAPRR 118
Db      293 VLANGNDNTIKERKHIDLDPS---KFGCDKNSVDVTWKMECCKPYKLSTKDVCPVPRR 349

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RESULT 10
US-10-293-913A-2
; Sequence 2, Application US/10293913A
; Publication No. US20040022805A1
; GENERAL INFORMATION:
; APPLICANT: Narum, David
; APPLICANT: Liang, Hong
; APPLICANT: Fuhrmann, Steve
; APPLICANT: Sim, B. Kim Lee
; TITLE OF INVENTION: Synthetic Genes for Malarial Proteins and Methods of Use
; FILE REFERENCE: 05213-0464 (43170-280206)
; CURRENT APPLICATION NUMBER: US/10/293,913A
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/345,051
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic EBA-175 RII
US-10-293-913A-2

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QY      359 SDEYRYCSRNGYDCEQTISRKGKVRMGKGTDCFFACGSYENWIDNRKQFQCK 414
      :      :      :      :      :      :      :      :      :
Db      514 EDD-----NCKRKNSYKEMISKKEEYNNQAK 541
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Query Match	13.8%	Score 292	DB 3	Length 1421
Best Local Similarity	23.8%	Pred. No. 3e-15		
Matches	99	Conservative	54	Mismatches 121; Indels 142; Gaps 17
QY	24	QKVHDEVGAQKANY---	VSELKGSLSIASILGETAFIVKSNQTE-SKY-	TELIEA 73
DB	387	QKVPRE--NAENYLKISKNKNAKAVSLT---	NNCDAESKYCDCKHHTTLTKS	436
QY	74	--NSGRNPCKKDGKNDVDRFSVGEQGYD-----	NKKMCSNGMTCAPYRR	118
DB	437	VLANGNDNTIKKREHIDLDDFS--KFGCDKNSVDNTNKKVECKKPYLSTFDVCPVPRR	493	
QY	119	LHLCKNFPNNNSNDSSKAKHDLTAELVMAKAYEGESIKTHYPKYDSKYPGSPDFMCTML	178	
DB	494	QELCLGNIDRIYDKNLMLIKHHILA---IMYBSRLIKRYKKNDDK-----	EVCKII 543	
QY	179	ARSPADIGDIRGADLYLGNKKKKKONGKETEREKLOQLKELFKKIHNLKDKNAQKRYN	238	
DB	544	NKTFADIDIIIGDIDYW-----NDLSNRKLVGKINTNSNYVHN--	KONDKLF- 589	
QY	239	GDEDPNFKLREDMWTANARETYMGAMTCSKELDNSSYFRATCNIDPGQSPSOTHNKRCDDK	298	
DB	550	-----RDEMKNVTKADVNVNT-----	SNVVK-----DKTYCKE 617	
QY	299	DKGANAGPKKAGDGVTITVPTFYEDVYPOLYRMFEEMAEADFCRKKKKKLENLBKQCRGDK	358	
DB	618	DDIEN-----IPQFWMFSEMGDYCODDKTKMLETLEKVECKEPC	657	
QY	339	SDEHYGCSRNGDEQGTISRKKGRVAMGSGCJDDCFAGCSYENMTIDNQRKQDDKOKK	414	
DB	658	EDD-----NCKRKNSSYKEMSKKKEETNKQAK	685	

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1      RESULT 12
2      US-10-153-273-6
3      ; Sequence 6, Application US/10153273
4      ; Publication NO. US20020169305A1
5      ; GENERAL INFORMATION:
6      ;
7      ; APPLICANT:  Sim, Kim L.
8      ;               Chitniss, Chetan
9      ;               Miller, Louis H.
10     ;               Peterson, David S.
11     ;               Su, Xin-zhaun
12     ;               Wellens, Thomas E.
13     ;
14     ; TITLE OF INVENTION:  BINDING DOMAINS FROM PLASMODIUM VIVAX
15     ;                       AND PLASMODIUM FALCIPARUM ERYTHROCYTE
16     ;                       BINDING PROTEINS

```

Query	March	Similarity	12.5%	Score	285.5	DB	4	Length	749
Match	Local	Similarity	24.1%	Pred.	No. 4.6e-15				
	89	Conservative	47	Mismatches	108	Indels	125	Gaps	16
Qy	69	ELIEA-----	NSKRNPKCKDGKGNVDREPSVEQAGYDKKKMC--	SNGMT-----	C	113			
Db	81	ELVSAKYNLAKPNAKSPRIYKSKHESSVYGCKTKI	SKYKKKNVCYNNKVTAPRQVVC			140			
Qy	114	APFRRLHC-NKNFNNMNSNDSSKKAHDLAEVCA	AAKTEGESITKTHPKYDSKTPGSDF			172			
Db	141	GPPRQOQCLGYIFLIRDGNBGLKDH-----	INFAANYEAMHLEKEK-----	ENAGD-		189			
Qy	173	PMCTMLASPADIGDIIRGRDLYLGNKKKKQKQNG	KEBERKLEQKKAIFPKHIDLKQKE			232			
Db	190	KICNAILGSIYADIGDIVRGLDW-----	RIINTKLSSEKQKIF-----	MGGN		233			
Qy	233	AQKRYNGEDENFYKLREDMWTANETWAGAMTCS	KELDNSSYFPAFCNDTGQGPSQTH			292			
Db	234	SRKQNDNNE-----	RNKWEKQNLIMSSWV--KHLPKGK--	TC-----	KRNH	273			
Qy	293	KCRCDKDKGAAGKPKAGDGVTVIPTYEDVYQYL	RPMPEEAEDPCKRKKKKLENLKQ			352			
Db	274	N-----	FEKLPFLRMKLEKGDFFCEMGTEVQKLEKI			306			
Qy	353	CRGKDKSDEYRYCSRNQYDCBOTISRKGKVRMGK	CTDCAFAGSYENWIDN-----	Q		405			
Db	307	CENKKCSK-----	KKNACSSYEKWKIKERKNEVNIQ			338			
Qy	406	RKQPDQKK	414						
Db	339	SKKFPDCK	347						

Query Match	12.5%	Score 285.5	DB 3	Length 1086	
Best Local Similarity	24.1%	Pred. No. 7.5e-15			
Matches	89	Conservative	47	Mismatches 108	Indels 125
				Gaps	16

Qy	69	ELI EA-----	NSKNPKCKDKGKNDVDRFSYKEQAGYNNKKKC--	SNGMT-----	113
Db	323	ELVAAAKYKYLKAPAKSPRIYKSEHESSVFGCKTKISKKKKWCNCKNNKVKTPGEGVC			382
Qy	114	APPRRLHC-NKNPNMNSNDSSKAKHDLALVCMALYEEGESI	KTHNPKTDSKPGSDF		172
Db	383	GPPRPQOCLCGLYTLIRDNKEGLKDH-----	INKAANYEAMHLEKY-----	ENAGSD-	431
Qy	173	PMCTMLARSPADIGDIIRGRDLYLGNNKKCKKNGKRETEKLE	BOXLKEI	FKKIHDLKDXE	232
Db	432	KICNALIGSYADIGDIYAGLDVW-----	RDINTNKLSEKFQKIF-----	MGAGN	475
Qy	233	AQKRYNGDEDEPFKTLREDWTANRETYWGMATSKSELDNS	YPPATCNDTNGQSPQTHN		292
Db	476	SRKKQNDNE-----	RNKWMEKORNLWSSMV--	KHLPKK--	Tt-----
Qy	293	KCRCDKDKGAAGAPKAGDGDDVTIVPTVFDVVPOLYLR	FEEMAEDEFCRKKKKLEMLEKO		352
Db	516	N-----	FEKILPQFLRWLKMGBGDFCGEMGTGVQLEKI		548
Qy	353	CRGKDKSDRYRYSRNGYDCEQTLISRKGLVBMGKGC	CTDPCFACGSYENWIDN-----	Q	405
Db	549	CENKNCSEK-----	KCKNACSSYERKMIKERNKNEYNIQ		580
Qy	406	RKQFDKQKX	414		
Db	581	SKKFDSDKX	589		

ADDRESSEE: Knobb Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California

```

COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/153,273
  FILING DATE: 21-May-2002
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/210,288
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Fuller, Michael
  REGISTRATION NUMBER: 36,516
  REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (619) 235-8550
  TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
  LENGTH: 921 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-153-273-8

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Query Match      10.6%; Score 241; DB 4; Length 921;
Best Local Similarity 26.1%; Pred. No. 3.5e-11;
Matches 84; Conservative 43; Mismatches 119; Indels 76; Gaps 17;

QY 101 DNKKKCSNGMTCAPRRHLCKNKFPMNNSNDSSKAGHDLAEVCMATYEGESIKTHY 160
DB 427 DESKIMQHGACIPPRQKCLHLEKIMTN-TLELKAFIK--CAAA--ETFLWQNY 481
QY 161 PK-----YDSKYPGSDFP--MCTMLARSPADIGDIIRGRDLYLGNKKKKQNGKETER 210
DB 482 KKDKNAGNABDEDEKLKGGIIFEDFKRMFYTFADYDICTGDI-----SSKKDTSKV-- 535
QY 211 EKLQKLEIKFKITDNLKDKAOKRYNGDEDPNPFYKLREDMWTANRETWGANMTCSEL 270
DB 536 GYVKNIDVDVFKYKINSI-----RY-----RKSWMETNGPVIWEGMLCALSY 577
QY 271 DNSSYFRATCNDTGGPSQTHNKCRCDDKGANAGKPRAGDGVTVITPFYDVPQYLRL 330
DB 578 DTS-----LNNVN---PETHKLL-----TEGNNNEKYIFGSDSTLTSKFSERQPIRL 624
QY 331 FEWMAEDFCRRKKKKLEMLEKQCRGKDKSDSEYRYSRNGYDCEQTISRKGYRMKGGCTD 390
DB 625 LTEMENFCFEQKKEKYKVLAKK-----DCD--VDGDKCN--GK--CVA 664
QY 391 CFFACGSYEN-----WIDNRKQ 408
DB 665 CKDQCKQYHSMIGIWDNYKQ 686

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```

RESULT 15
US-10-153-273-2
Sequence 2, Application US/10153273
Publication No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Slim, Kim L.
            Chitnis, Chetan
            Miller, Louis H.
            Peterson, David S.
            Su, Xin-zhaun

```

```

Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/153,273
  FILING DATE: 21-May-2002
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/210,288
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Fuller, Michael
  REGISTRATION NUMBER: 36,516
  REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (619) 235-8550
  TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  LENGTH: 1115 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium vivax
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-153-273-2

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Query Match      10.5%; Score 239; DB 4; Length 1115;
Best Local Similarity 21.4%; Pred. No. 6.6e-11;
Matches 94; Conservative 59; Mismatches 153; Indels 134; Gaps 17;

QY 5 GGSGGTODEDAKHVLDLDFGQKVHDEVHGEAK--NYVELGSLSLASLTGTAFTVSKWQ 62
DB 157 GGNYSMEGKDG-----GDKTGEKDGDEHKTDSKTNGKANLVMLDIETSSNGQPA 209
QY 63 TESKYTELLI---EANSKRNPKCKDKGKNDVD-----RFSYKQAGYDNKK 104
DB 210 TLIDVLEFVYGHENSKRN--SSNGNPNYDIDHKTTISSALINHAFLQNTVWKNCKNYRKR 268
QY 105 MK-----CSNGM--TCAPRRHLCKNKFPMNNSNDSSAKHD-----LAEVCMATY 152
DB 269 RERDMDCNTKQDVCI PRRRYQLCKMKELTNLVNNTDTFHRITPRKLYLKKKLYYDAVE 328
QY 153 GE-SIKTHYPKYDSEYRYSRNGYDCEQTISRKGYRMKGGCTD 210
DB 329 GDLILKLNRYRN-----KDF--CKDIRWSLGDGDIIMGTDMGIGISK----- 371
QY 211 EKLQKLEIKFKITDNLKDKAOKRYNGDEDPNPFYKLREDMWTANRETWGANMTCSEL 270
DB 372 -VVENNLRSIFG-----TDEKAQR-----RQGMNBSKAQIWTAMMYSVKK 412
QY 271 DNSSYFRATCNDTGGPSQTHNKCRCDDKGANAGKPRAGDGVTVITPFYDVPQYLRL 330
DB 413 RLKGNFIWICK-----LNVAVNIEPQIYRW 437
QY 331 FEWMAEDFCRRKKKKLEMLEKQCRGKDKSDSEYRYSRNGYDCEQTISRKGYRMKGGCTD 390

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Db	438	IREWGRDYVSELPTEVQKLKEXCDGKINYTDKXCK	-----VPP	476
Qy	391	CFPAGSYENMIDNRKQED		410
Db	477	CONACKSYDQWITRKKNQMD		496

Search completed: December 29, 2005, 23:40:11
Job time : 47.2601 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 23:15:22 ; Search time 2.64597 Seconds
(without alignments)
1174.559 Million cell updates/sec

Title: US-09-508-967-1_COPY_1_415
Perfect score: 2276
Sequence: 1 MATSGSGSGGTDEDAKHVLD.....GSYENWIDNRKQKQKQKY 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA New:*
1: /cgm2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
2: /cgm2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
3: /cgm2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgm2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgm2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgm2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgm2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgm2_6/ptodata/2/pubpaa/US66_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	111.5	4.9	454	US-11-089-551A-35	Sequence 35, Appl
2	102.5	4.5	1147	US-10-615-668-5	Sequence 5, Appl
3	101	4.4	1142	US-11-109-156-22	Sequence 22, Appl
4	99.5	4.4	1976	US-11-069-834-52	Sequence 52, Appl
5	98.5	4.3	646	US-10-491-096-190	Sequence 190, App
6	95.5	4.2	1976	US-11-069-834-54	Sequence 54, Appl
7	93.5	4.1	835	US-10-501-039-4	Sequence 4, Appl
8	93.5	4.1	1238	US-11-078-735-21	Sequence 21, Appl
9	93.5	4.1	2897	US-10-499-715-2	Sequence 2, Appl
10	92	4.0	785	US-11-109-157A-6	Sequence 6, Appl
11	92	4.0	1076	US-11-109-157A-6	Sequence 6, Appl
12	92	4.0	1907	US-11-039-398-25	Sequence 25, Appl
13	91.5	4.0	989	US-10-793-626-2594	Sequence 2594, Ap
14	90.5	4.0	567	US-10-995-561-764	Sequence 764, App
15	90.5	4.0	619	US-10-485-517-374	Sequence 374, App
16	90.5	4.0	791	US-11-056-621-4	Sequence 4, Appl
17	90.5	4.0	810	US-10-995-561-761	Sequence 761, App
18	90.5	4.0	810	US-10-220-824-2	Sequence 2, Appl
19	89.5	3.9	436	US-10-131-826A-404	Sequence 404, App
20	89.5	3.9	948	US-10-523-477-14	Sequence 14, Appl
21	88.5	3.9	963	US-10-467-962B-2	Sequence 2, Appl
22	88	3.9	477	US-11-089-551A-34	Sequence 34, Appl
23	88	3.9	636	US-10-485-517-170	Sequence 170, App
24	87.5	3.8	558	US-10-512-109-11	Sequence 11, Appl
25	87.5	3.8	710	US-11-045-802-2	Sequence 2, Appl

26	87.5	3.8	710	US-11-045-802-19	Sequence 19, Appl
27	87.5	3.8	710	US-11-045-802-20	Sequence 20, Appl
28	87.5	3.8	710	US-11-045-802-21	Sequence 21, Appl
29	87.5	3.8	710	US-11-045-802-22	Sequence 22, Appl
30	87.5	3.8	710	US-11-045-802-24	Sequence 24, Appl
31	87.5	3.8	812	US-11-010-874-1	Sequence 1, Appl
32	87	3.8	812	US-11-045-802-23	Sequence 23, Appl
33	87	3.8	1960	US-11-069-834-50	Sequence 50, Appl
34	85.5	3.8	369	US-11-078-735-38	Sequence 38, Appl
35	85.5	3.8	484	US-11-078-735-43	Sequence 43, Appl
36	85.5	3.8	531	US-11-060-914-4	Sequence 4, Appl
37	85.5	3.8	723	US-10-131-826A-346	Sequence 346, App
38	85.5	3.8	723	US-11-078-735-17	Sequence 17, Appl
39	85.5	3.8	763	US-10-821-234-1619	Sequence 1619, Ap
40	85	3.7	557	US-10-512-109-9	Sequence 9, Appl
41	85	3.7	793	US-11-060-914-2	Sequence 2, Appl
42	84.5	3.7	603	US-10-793-626-1684	Sequence 1684, App
43	84.5	3.7	693	US-10-873-735-185	Sequence 185, Appl
44	84.5	3.7	1218	US-11-078-735-20	Sequence 20, Appl
45	83	3.6	399	US-10-510-386-150	Sequence 150, App

ALIGNMENTS

RESULT 1
US-11-089-551A-35
; Sequence 35, Application US/11089551A
; Publication No. US20050266242A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al.
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40025A
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US/11/089, 551A
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-089-551A-35

Query Match 4.9%; Score 111.5; DB 7; Length 454;
Best Local Similarity 21.2%; Pred. No. 0.072;
Matches 86; Conservative 40; Mismatches 147; Indels 133; Gaps 20;

QY	35	KNY	-----VSELKGSLSLASIIIGETAFYVSKMOTESKYTELIEANSKRNPCKDGKGVDR	91
DB	16	KGY	YKNSNSGSGSGSDVSGTNGSNKAKNTYKKT-----NKK--YKATDKANDTKY	67
QY	92	FS	-----VVEQAGYDKKIKKCSNGMTCAFRRLHLCKNFKPMNSN-----DSSKAKIDL	141
DB	68	YSN	KKSKRSKNSNSNDKDC-----RTTNQDMTYDKSKVTNCDHAKSSSM	115
QY	142	LA	YCAKKEGESI-KTHYPKYDSKYPGSDFPYCMLARSFADIGIIRRDLY----	196
DB	116	-----	KYKRSVVDKHWKDDSVYAS-----KNNSHYST--NTMNRMDDVYTKAM	160
QY	197	G	KKKKKNGKTEBEKLEQLKELFKKIHDLKDKKQKRYNGDDEPFYLRBDWWTAN	256
DB	161	ANK	KK-----SPTSTWKNKNSHVSYN-----NDKSKTKMTNDDDDNNVNNNNNN	210
QY	257	RET	WAMTCSKEIDNSYFRATCNDTGQSPSQTIN-----KCRCDKGCANAGK	306
DB	211	-----	NKDNNDNNNDTSMNNNNNNNNRKNRNNRNDWTKKCTDWDNDKRDNNK	260
QY	307	PK	AGDVTIPTYTFDYVPQRLRWFEEAEPFCRKKKKLENLKQCKGKSKSDEYRCS	366
DB	261	-----	NMAENDKNNVNNVR--NHKSS-----CR	284

QY 367 RAGYDCEQTI-----SRKGYVMGKCTDCEPACGSYEMWIDNORK 407
 Db 285 RDGYSANNAVSTHASNKNVDMNN-----DTYGNKTDYMKK 321

RESULT 2

US-10-615-668-5
 ; Sequence 5, Application US/10615668
 ; Publication No. US20050276819A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Covacci, Antonello
 ; APPLICANT: Bugnoli, Massimo
 ; APPLICANT: Telford, John
 ; APPLICANT: Macchia, Giovanni
 ; APPLICANT: Rapinoli, Rino
 ; TITLE OF INVENTION: Helicobacter pylori CAI Antigen Polynucleotides
 ; FILE REFERENCE: CHIR0337
 ; CURRENT APPLICATION NUMBER: US/10/615,668
 ; CURRENT FILING DATE: 2003-07-08
 ; PRIOR APPLICATION NUMBER: 08/471,491
 ; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: 08/256,848
 ; PRIOR FILING DATE: 1994-10-21
 ; PRIOR APPLICATION NUMBER: 09/410,835
 ; PRIOR FILING DATE: 1999-10-01
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 5
 ; LENGTH: 1147
 ; TYPE: PRT
 ; ORGANISM: Helicobacter pylori
 US-10-615-668-5

Query Match 4.5%; Score 102.5; DB 6; Length 1147;
 Best Local Similarity 20.4%; Pred. No. 1.2; Indels 119; Gaps 23;
 Matches 94; Conservative 69; Mismatches 178;

QY 1 MATSGSGGTODEDAKHVLDYDFGQKVDHVEHGAKNVYSELKSLSLASIIGETAFYTKS 60
 Db 457 LITTEFGNG-----DLSYTKDYKQKA-DKALDREKNVT--LOGSLKHGVM----FVYYS 504
 QY 61 MOTESKYTELLEANSKRNPKCKDGNVDYRPSVKEQAGYDNK---KMKCSNGMTCAPF 116
 Db 505 ---NFKYT-----NASKNPNKGVGTNGVSHLEV---GF-NKVALIFMLPDLNMLAITSF 551
 QY 117 RLHLCKN-NFPNNNSNDSSKAKHDLAEVCMAYKBEGSITHTHPYXDSKYRPSGDFPMC 175
 Db 552 VARNLEDKLTTRKGLSPQEAANKLIKDFLS--NKELVGKTLNFKRAVADAKVTGN---Y 604
 QY 176 TWLASFADIGDIIIGRDLYLGNKKKKQNGKETEREKLEOKLK-----EIF----- 221
 Db 605 DEVKKAQKDLESLAKREHLEKEVERKLESKGNKNKMEAKQAQANSQDEIFALINKKAN 664
 QY 222 -----KKIHDLK--DYEAQRVNGDEDPNFYKLRBDW----- 252
 Db 665 RDAARAIVAQNLKGIKRELSDKLENNVKNLKDPDFSKDEFKNG-KKQDFSKAEFTLKALK 723
 QY 253 -----WTARETWGAMTSGKELDSSYFRATNDTGQSPQSTHMKR----- 295
 Db 724 GSVKDLGINPEWISKVENLNAALNFKNGKNKDFSVT-----QAKSDLENSVKVITINQ 778
 QY 296 --CDKDKANAGKPKA-GGDVTVIVPTVFDYVPOYLPMPEBMAEDFCRKKKKLENLKQ 352
 Db 779 KYTDKNDINQAVSAKATGD-----FSRYEQALADLKNFSKQQLAQQAQKESL--- 828
 QY 353 CRGKDKSDEYRYCSR--NGYDCEQTI SRKGYVMGKCTD 390
 Db 829 -NARKKSEIYGSYKNGVNGTLVNGLSQAEATTLISNFSQ 867

RESULT 3
 US-11-109-156-22
 ; Sequence 22, Application US/11109156

; Publication No. US20050250144A1

; GENERAL INFORMATION:
 ; APPLICANT: Toshio Ota
 ; APPLICANT: Takao Isegaki
 ; APPLICANT: Tetsuo Nishikawa
 ; APPLICANT: Koji Hayashi
 ; APPLICANT: Kaoru Otsuka
 ; APPLICANT: Jun-ichi Yamamoto
 ; APPLICANT: Shizuko Ishii
 ; APPLICANT: Tomoyasu Sugiyama
 ; APPLICANT: Ai Wakamatsu
 ; APPLICANT: Keiichi Nagai
 ; APPLICANT: Tetsuji Otsuki
 ; APPLICANT: Shin-ichi Funahashi
 ; APPLICANT: Chiaki Senoo
 ; APPLICANT: Jun-ichi Nezu
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
 ; FILE REFERENCE: PHOSPHATASE
 ; CURRENT APPLICATION NUMBER: US/11/109,156
 ; CURRENT FILING DATE: 2005-04-19
 ; PRIOR APPLICATION NUMBER: US/10/060,065
 ; PRIOR FILING DATE: 2002-01-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/05061
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/159,590
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: US 60/183,322
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: JP 11-248036
 ; PRIOR FILING DATE: 1999-07-29
 ; PRIOR APPLICATION NUMBER: JP 2000-118776
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: JP 2000-183767
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: JP 2000-241899
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 22
 ; LENGTH: 1142
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-109-156-22

Query Match 4.4%; Score 101; DB 7; Length 1142;
 Best Local Similarity 22.9%; Pred. No. 1.6; Indels 158; Gaps 25;
 Matches 81; Conservative 40; Mismatches 74;

QY 102 NKKMKCSNGMTCAPFRLHLGN-----KNFPNNNSNDSSKAKHDLAEVCMAYKRG-- 153
 Db 214 NKSIRQNLTL-----KRRINNVFKDFLKEFNNTICDSSVSTHDL-----KVKYIATL 262
 QY 154 ESITHTYPKIDSKTPGSGDFPCTMLARSFA-----DGGDIIIGRDLYLGNK-----K 200
 Db 263 ETLTKHY-----GAEIFETSMILLISSENNMWFHSNCGANLYYEVMVWGIGIQMR 314
 QY 201 KKONGKETEREKLEOKLEIFKKIHDNLKDEQAQRYNGDEDPNFYKLRBDMTAN----- 256
 Db 315 HKPWNVSVEKKE--NKLKR--KLEEN--KDKK-----DEKKA--KIREEMNNFSPPE 359
 QY 257 -----RETVGAMTSGKELDN-----SSYFRAT-----CNDT 283
 Db 360 ITHIVIKESV--VSINKQ-DNKQWELKLSHEBALSFVSLVDGYFRLTADAHNYLCTDV 415
 QY 284 G-----QGPSQTH--NKCRCDKKGANAGKPKAGDDVTVIVPTVFPYVPOYL 328
 Db 416 APPLIVHNIGQCHGPICTEYAINKLR--QEGSEBGH-----YV---L 453
 QY 329 RMPEBMAEDF-----CRKKKKKLENLKRCR-----GKDKS 359
 Db 454 RMS---CTDFDNIIMTYTTCFEKSEYQGAQKQFKNFQIEVQKGYSLHGSIRS 503


```

RESULT 4
US-11-069-834-52
; Sequence 52, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS D.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; PRIOR FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: 60/588,648
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
; LENGTH: 1976
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-069-834-52

Query Match          4.4%; Score 99.5; DB 7; Length 1976;
Best Local Similarity 17.1%; Pred. No. 4; Indels 57; Gaps 8;
Matches 54; Conservative 62; Mismatches 143;

QY 11 QDEDAKHYLDFGCGVHDEHGEAKNYVELKSLSLASIIIGETAFTVSKMOTESKYTEL 70
DB 991 EDQSKPIFKER-KLMERIRAECSQLAEBEEXAKNIAKINRKGVMISDLBRLKKEK 1048
QY 71 IEANSKRNPKCKDGKNDVDRPSVEQAGYNDKKKCS-----NGMTCAPPRILHLCKN 124
DB 1049 TROSELEKARKLDGGSTTDLQDQIAELQAVDELKQVLTKKEBELQGA-----LARG 1099
QY 125 NFPMMNSDSSAKHDLAEVC-MAKYEAGESIKTHPKYDSKYPGSDFPMTMLARSFA 183
DB 1100 DDETHAKNNALVARELQAIAELOEDPESEKASRNKAKEKOR-----1142
QY 184 DIGDIIIRGRDYLGNKKKKKQKETEREKLEQKLKEIFPKIHDNLKDEAKRYNGDEDP 243
DB 1143 DLSELELKTLEBETDITLTAQDELTKRGEQVAVELKKALADETRKHEAQ-----1193
QY 244 NFYKLREDWMTANRETVGAMTCSKELDNSSFPRATCNDTQGSQTHNKCRC-----K 298
DB 1194 -IQMRQGHATALEB-----LSFQLQAKRFKANKLEKNKQLETDNKELEACEVKVLQ 1245
QY 299 DKGANAGPKAGDDGV 314
DB 1246 VKASEHRRKKLDAQV 1261

RESULT 5
US-10-491-096-190
; Sequence 190, Application US/10491096
; Publication No. US20050267020A1
; GENERAL INFORMATION:
; APPLICANT: FAURE, OLIVIER
; APPLICANT: KOSMATOPOULOS, KONSTANTINOS
; TITLE OF INVENTION: POLYPEPTIDES DERIVED FROM INDUCIBLE HSP70 AND PHARMACEUTICAL
; FILE REFERENCE: 0508-1098
; CURRENT APPLICATION NUMBER: US/10/491,096
; PRIOR FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10821
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: FR 01402496.2
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190

```

```

; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-491-096-190

Query Match          4.3%; Score 98.5; DB 6; Length 646;
Best Local Similarity 20.0%; Pred. No. 1.2;
Matches 106; Conservative 78; Mismatches 200; Indels 145; Gaps 25;

QY 14 DAKH-----VLDFEQG-KVHBEVGEAKNYVELKSLSLASI-----LGET-----54
DB 86 DKHMPMTVVNDAGRPVQVEYKGETSYFEEVSSWVLTTRMKIAEYLAGKTYTNVAVT 145
QY 55 -AFTVSMOTESKYTEL1-----EANSKRNPKCKDGKNDV 89
DB 146 VPAYFNDSQOQATDAGTIAGLAVTLRIINEPTAAIAVAGDJKYAGARNVILFPLGGGT 205
QY 90 D-----RFSYEQAG-----YDNKKMKCSGMTCAPPRILHLCKNFPNMNSN 132
DB 206 DVSILTTIEDGIFEVKSTAGDTHLGGEDFDNRMV-----NHFAEFKRKH-----KK 251
QY 133 DSSAKHDL--LAEVCMAKYEAGESIKTHPKYDSKYPGSDFPMTMLARSFAD1-GDII 189
DB 252 DISENKAVALRLTACERAKRTLSSSTQASIEIDSLVEGIDFYTSTRAR-FEELANDLF 310
QY 190 RG-----RDLYLGNKKKKON-----GKETEREKLEQKLKEIF--KIHNDLKDEA- 233
DB 311 RGTIDPPEKALRDAKL-DKSGIHDIVLVGSGSTRIPKIQKLQDFPNKELEKINSINPDEAV 369
QY 234 -----QKRYNGEDBN---FYKLREDWMTANRETVGAMTCSKELDNSSFPRATCNDT 283
DB 370 AYGAAVOAALISGDKSENQDILLDVTPLSLGIETAGVMTVL1KNTVTIPKOTOTFT 429
QY 284 GQGSQTHNKCRC-DKXGANAGPKAGDGVITVPTFYFDVPOYLAHFEEMA-----335
DB 430 TYSNQGVLIVYEGGRAMTKNNLKGKELTGIIPAPRGVPOIEVTFTDANGILNVS 489
QY 336 -----EPCFRKKKKLENLKQC-----RGKDSDRYCSRN-----GYDC 372
DB 490 AVDSKTEKENKITTTNDKRLSKEDIERMVOEAKRYAEDBKODKYSKKSLSYAFNM 549
QY 373 EGTI---SRKGKVMGKCTDCCFPAGCSYENMIDN---ORKOPDKK 414
DB 550 KATVEDKLGKIN-DEDKQILDKNEIINWLDKNQTAKEBEFEHQK 597

RESULT 6
US-11-069-834-54
; Sequence 54, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS D.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; PRIOR FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: 60/588,648
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 54
; LENGTH: 1976
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-069-834-54

Query Match          4.2%; Score 95.5; DB 7; Length 1976;
Best Local Similarity 16.8%; Pred. No. 8.4;
Matches 53; Conservative 63; Mismatches 143; Indels 57; Gaps 8;

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OY      1  ODEAKHYLDSEFGQVHVEHVEAGNANYVELKXGSLSLIIGETAFTVKSQOTSXYEL  70
Db      991  EDQNSKFIEXK-KMEDRIACSSQLABEEBKANLAKINRQEWMSIDLEERIKXEK  1048
OY      71  IEANSKRNPCCKDGKNDVDRFPSVYEQAGYDNKKKCS-----NGMTCAEFRRLHLGNK  124
Db      1049  TRQELERAKRKLDTGGTTLTDQDQIAEQIDELKQLAKKEEELQGA-----LARG  1099
OY      125  NFPNNNSDSSKAKHDLIAEVC-MAKYEGBSIKTHYPRYDSKYPGSDPMPCTMLARSFA  183
Db      1100  DDETLHKNNALKVAVELQAIQIAELQEDFESEKASHNKAQKR-----  1142
OY      184  DIGDILIRGDIYGNKKKKQKQNGKLETEREKLEBQKLKEIFKLIHDNLKQXEAQRYGDEDP  243
Db      1143  DLSELEELAKTELBEITLDTLTAQQELRTKRBEVEVALKALBEETKXNHEAQ-----  1193
OY      244  NPYKLRBDMWTANRETTWGAFTCSKELNNSYFRATCNDTGGQSPSQTNKRCQD-----K  298
Db      1194  -IQQDRQHHATLAE-----LSQLOQAKRFKALNEKNQGLETTDNKELACEVYKLOQ  1245
OY      299  DKGANAGKPKAGDDGV  314
Db      1246  VKAEBEHKPKKLDAQV  1261

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RESULT 7
US-10-501-039-4
; Sequence 4, Application US/10501039
; Publication No. US2005024482A1
; GENERAL INFORMATION:
; APPLICANT: Tetsuro Kokubo, Masahiro Shirakawa, and Jeremy Robin Howard Tamea
; TITLE OF INVENTION: Method of monitoring gene expression
; FILE REFERENCE: 4439-4023
; CURRENT APPLICATION NUMBER: US/10/501, 039
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: JP P2002-002396
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 835
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-501-039-4

```

Query Match 4.14; Score 93.5; DB 6; Length 835;

Best Local Similality 15.2%; Freq. NO. 4.2;
Matches 92; Conservative 59; Mismatches 142; Indels 187; Gaps 22;

```

0Y      13 E0AKVILDFGQKVHDEHVGKANNVYSELKGSILSLISIGETAFYKSMQTESKYTELLE 72
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      201 EDASRKSXYFW--VHDDNIMEVKARILRLPALVYASVENENDPFDNLESVDVROVPEAR 258
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y      73 AN--SKRNPCKQKGN-----DVRFVYKQAGYDNKK 104
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      259 IINGKSNLSLSDGNSMDVEIGKSKSVIFPOSYDPTITLTYEPDNDFDL-----YNRRK 313
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y      105 MKCSQMGTAPPRRLTLGNK--NPKM-----NSNDSKAKDDLAEVCMAKARYEG 153
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      314 LKISG----APLRLRLMIGKLDKPIPLEKRTFMENTGNSPFEIRLQ--MKAKFIN 367
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y      154 BSIKTHYPYDSKYPSQSDPMPCTMLARSPADIGDILRGDLVYGNKKKKONGKETEREKL 213
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      368 NFIKNQDPSYKN-----YLINLIREG--TQKEEL 395
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y      214 E0LKEIFPKIHDLNKKQEAQ---KRYN-----GDE-----DPNFKLREDMWTAN 256
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      336 E-KLSRDFPNIGNFIYERKLQPLRATRYRIRTAQIIGDQSIKVTIDSNIMYIRREDSLDRN 454
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y      257 RETTWGAMTCSKELDNSSYFRATCNDTGGQSPQSTENKCRCDKXKANAGKP-----KAQD- 311
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      455 RFI-----NPNEMWR-----DDIDSNINPPLFELAGEK 484
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Oy	312	-----GGVTVPTV-----	FDVYPQ-----	YLR-----	329
Db	485	SKPPYSVMEIKVIYNDQNSQMPPYEWIKDUTNSHLVNEVPKPSLYLQGVASLFGEDDKYNN			544
Oy	330	-----WEEBAEDPCKKKKKLE-----	NLEKCRGDKSDDEVRYRSRNGYDCEQIISRKQ		381
Db	545	ILPFWMLPDETDIRKPKQPEAYEEKKTLQKQSIHDKIDNNKRLSKISVDPDKTTKEQQ			604

RESULT 8
US-11-078-735-21

Publication No. US20050261477A1
GENERAL INFORMATION:
APPLICANT: CHAMPTON, BRIAN ROBERT
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: MCKENZIE, GRAHAME JAMES
APPLICANT: TUGAL, TAMARA
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
TITLE OF INVENTION: COMPISING NOTCH LIGAND PROTEINS

```

/ CURRENT APPLICATION NUMBER: US/11/078,735
/
/ CURRENT FILING DATE: 2005-03-10
/
/ PRIOR APPLICATION NUMBER: PCT/GB03/03908
/
/ PRIOR FILING DATE: 2003-09-09
/
/ PRIOR APPLICATION NUMBER: PCT/GB03/03285
/
/ PRIOR FILING DATE: 2003-08-01
/
/ PRIOR APPLICATION NUMBER: PCT/GB03/01525
/
/ PRIOR FILING DATE: 2003-04-04
/
/ PRIOR APPLICATION NUMBER: GB 0300234.2
/
/ PRIOR FILING DATE: 2003-01-07
/
/ PRIOR APPLICATION NUMBER: PCT/GB02/05117
/
/ PRIOR FILING DATE: 2002-11-13
/
/ PRIOR APPLICATION NUMBER: PCT/GB02/05133
/
/ PRIOR FILING DATE: 2002-11-13
/
/ PRIOR APPLICATION NUMBER: GB 0220912.0
/
/ PRIOR FILING DATE: 2002-09-10
/
/ PRIOR APPLICATION NUMBER: GB 0220913.8
/
/ PRIOR FILING DATE: 2002-09-10
/
/ NUMBER OF SEQ ID NOS: 51
/
/ SOFTWARE: PatentIn Ver. 3.3
/
/ SEQ ID NO: 21
/
/ LENGTH: 1238
/
/ TYPE: prt
/
/ ORGANISM: Homo sapiens
/
US-11-078-735-21

```

Query Match	Score	DB	Length
4.18;	93.5;	7;	1238;

Match	Conservative	Mismatches	Indels	Gaps
39	25	65	67	9

```

QY      253 TTANEEYWGAMTCKSELD-----NSSEFPATCNDUQGSQOTHNCR 295
Db      291 WQCNSEITWGGLCCKDLNYGCSHHPTCTNGTCTINAEPPQYRCTCPDYSIGN----- 343
QY      236 CDKDKGANAAGKPKAGDGDVTIVPYFD--YVPOYLEW-----FEEMAEDFCRKKKKKL 346
Db      344 CEKAHACTSNPCANGSGCHEVPSFEGCHPS--GMSGPTCLDIDECASNPCAAAGTCV 401
QY      347 ENLE-----KCRGKDKSDEYR-----YC-----SRNGVDCBOT 375
Db      402 DQVDDPECTCEPQWGWATCQDLDAEBCBGRPCINAFSCSKLLGGYYCDCLPMKGINCHIN 461
QY      376 ISR--KGKVRMGKCTD 390
Db      462 VVDCRGQCOHGGCTKD 477

RESULT 9
US-10-499-715-2
; Sequence 2, Application US/10499715
; Publication No. US20050250717A1

```

```

GENERAL INFORMATION:
APPLICANT: BENYAHU, Dafna
TITLE OF INVENTION: CHROMATIN REMODELING PROTEIN AS A MARKER EXPRESSED BY STROMAL PRO
FILE REFERENCE: BENYAHU=1.1 PCT
CURRENT FILING DATE: 2004-06-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 2897
TYPE: PRT
ORGANISM: Homo sapiens
US-10-499-715-2

Query Match      4.1%; Score 93.5; DB 6; Length 2897;
Best Local Similarity 19.7%; Pred. No. 19;
Matches 72; Conservative 62; Mismatches 163; Indels 69; Gaps 13;

QY      13 EDAAKAVLDFGQKVDVHGEAKNYSELKGSLSLISLIGETAFYVKSMTESKTELIE 72
DB      426 DNSSHILP-----HDLRQFTSHL---VTRPSDMAQOTLOQOARSWHSFSPNRQH 472
QY      73 ANSKXNPP-----KKDGK-----NDVDRFSVYEQ---AGYNNKKKKKCSNGMTC 113
DB      473 LHDRHLLCQROPSSKSSDSGTYTKLQNTQVRVMSKKQKKVSESSKQKKANRITSE 532
QY      114 AFRRLHLCKNPFPMNSNDSSKAKHDLAEVCMAYKEGESIKTHYPTKSDKPSGDFP 173
DB      533 AIAKAKGERGNIPIVMSPEPNPT-----ASYEGKEKKGRMKSPKPKDQSKTKYT--- 584
QY      174 MCTMLARSPADIGDIRGDLVGNKKKKKQNGKREKLEKKEIKFIKHIDNLDKQEA 233
DB      585 -CSKTL-KERTKIGKLI---ITLGKKOKRKNESSDEISDAECPH-----TLKDDDS 631
QY      234 QKRVGDDDPNFYKLRDMWTANRETVGAMTCSKELNNSYFRATCNDTGGQPSQ--- 289
DB      632 QKGRNROIKRKKYAEIDEGKQSEEVKSKMKIK--NSAPL-----PGEPLQLVVE 682
QY      290 ---TNNKCRCDKDGKAGKAPKAGDGVTVIPTYVYVQVLRWFENAEPCFKKKKKL 346
DB      663 NPSEDAIVDKILSSRTYKKEISPGWIDTEEFVTKKNTSYLHCENATEEQLLKDKRI 742
QY      347 ENLEKQ 352
DB      743 QOKIKR 748

RESULT 10
US-11-109-157A-6
Sequence 6, Application US/1109157A
Publication No. US20050277175A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: TRUNCATED ADAMTS MOLECULES
FILE REFERENCE: 0197.030500.
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/562,685
PRIOR FILING DATE: 2004-04-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 785
TYPE: PRT
ORGANISM: homo sapiens
US-11-109-157A-6

Query Match      4.0%; Score 92; DB 7; Length 785;
Best Local Similarity 20.2%; Pred. No. 5.1;
Matches 92; Conservative 54; Mismatches 138; Indels 172; Gaps 26;

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```

QY      11 QDEDAKAVLDFGQKVDVHGEAKN--YSELKGSLS-----LASLIGETAFYVKSMTQ 62
DB      363 RDEQCAH-----FDCK-HENINGLLPNVRWVVKYSGILMKDRCKLFCRVAGNTA----- 410
QY      63 TESKYTELIANSKRNPKCKDGKNDVDRFSVKEQAGYDNKKMKCSNGMTCAPFRRLHLC 122
DB      411 ---YQLRDRVIDTGPCGD--TNDICVQGLCRQAGCD-----HVL 446
QY      123 NKNFPMNMSNDSSKAKHDLAEVCMAYKEGESIKTHYPKYDSKYPSGDFPM----- 174
DB      447 N-----SKARRD---KCGVCGGDSCKTVAGTNTVYVGNVTRIPAGATN 491
QY      175 CTMLARSPADIGD-----IIRG-----RDLVGNKKKKKONGKET--ER 210
DB      492 IDVAGHSFGSETDDDNVTLALSSKGEFLNPNFVYAKREIRIGNAVVERSGSETAVER 551
QY      211 ---EKLEQKKEIFPKKHIDNLDKQEAQRYNGEDPNFY---KLRDMWTANRETVW 261
DB      552 INSTDRIEQELL-----LQVLSVGKLYNPVRYSFNPIEDKPOQFYW--NSHGPW 600
QY      262 GAKTCSKELNNSYFRATCNDTGGQPSQTHNKCRCDK-DKGANAGKPAKAGDGVTVIPTY 320
DB      601 QA--CSKPCQGERKRLVC--TRESDDLTVSDQRCRLPQGHITTEPGTCD----- 649
QY      321 FDVYPOYLRFW-----LRMVVASRSECSAOGGLGYRTLIDYCAKYSRLDQKTEKVDVDFCSHPKP--SN 701
DB      650 -----LRMVASRSECSAOGGLGYRTLIDYCAKYSRLDQKTEKVDVDFCSHPKP--SN 701
QY      349 LEKQCRGKDSDEYRY-----CSRNGYDCQGTISRK 379
DB      702 REK-CSGECNTGGMWRYSAMTECSKS---CDGQTORR 733

RESULT 11
US-11-109-157A-5
Sequence 5, Application US/1109157A
Publication No. US20050277175A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: TRUNCATED ADAMTS MOLECULES
FILE REFERENCE: 0197.030500.
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/562,685
PRIOR FILING DATE: 2004-04-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 1076
TYPE: PRT
ORGANISM: homo sapiens
US-11-109-157A-5

Query Match      4.0%; Score 92; DB 7; Length 1076;
Best Local Similarity 20.2%; Pred. No. 7.5;
Matches 92; Conservative 54; Mismatches 138; Indels 172; Gaps 26;

```



```

; Sequence 764, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 764
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-764

Query Match          4.0%; Score 90.5; DB 6; Length 567;
Best Local Similarity 19.4%; Pred. No. 4.5;
Matches 83; Conservative 51; Mismatches 148; Indels 145; Gaps 22;

QY 25 KVHDEVHGAKNYSELK-----GSLSLASILIGETAFTVKSMTESKY----- 67
DB 87 RMRDVVLEKKVYLSECKTGNGKNYRGTMSTK---KNGITCQKWSSTSPRRPRSPATH 142
QY 68 -TELEANSKRNPKCKDGK-----NDVDRFSVKEQA-----GYDNKMKCS 108
DB 143 PSEGLEENYCCNRP-DNDQGPWCYTTTDEKRYDYCDILECEBECMHCSENGENYDGIKSTKM 201
QY 109 NGMTCAPRRLHLCNKNPNNNSNDSSKAKHDLAEVCMARKYEGESIKTYPKY----- 163
DB 202 SGLSCQAW-----DSQSPH---AHGITPSKFPKNLKKNYCNRPPREL 241
QY 164 -----DSKYPSGSDPFCMTMLARSPADIGIIRGR-DLYLGNKKKKONGKETEREKL 213
DB 242 RPMCFTTDPNKRMEICDIPTCTTPPSGSPYQCLKNGENYRGVAVTAGHTCQH--W 299
QY 214 EQLKEIKFKIHDNLKDKKAEQKRYNGDEDPNPKLREWM-WTANRETWG----- 262
DB 300 SAQTPHTNRPENFPCKNLDENYCRNPDGK---RAPWCHTINSQVWMEYCKIIPSCDS 355
QY 263 -----AMTCSKEL-----DNSSYFRATCNDTGOG-----PSOTHNKCRCDKD 299
DB 356 PVSTEQIAPPELTPVYVOCYHGDGQSY-RGTSSTTTTGKCCQSSMTPPHRQKTPR 414
QY 300 KGANAG-----XPKAGDGVTVTPYFDYVPQYLRFEEWABDFCRKKKKKLENLEKQ 352
DB 415 NYRNAAGLTMNYCRNPDADKG-----PWCFTTDPG-VRW-----EYCNLKK----- 453
QY 353 CRGKDKS 359
DB 454 CSGTEAS 460

RESULT 15
US-10-485-517-374
; Sequence 374, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexue Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629MO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 374
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-374

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Query Match          4.0%; Score 90.5; DB 6; Length 619;
Best Local Similarity 19.1%; Pred. No. 5;
Matches 66; Conservative 47; Mismatches 138; Indels 95; Gaps 15;

QY 41 LKSLASILIGETAFT-VKSMOTESKYTELEANSKRNPKCKDGKGNVDVRFVKEQAG 99
DB 11 LSTLVLPVIVSPAYADTPQKDTAKTSHDSKSSNDDETSKDTSDIKADKNNTSN 70
QY 100 YDN--KKMKCSNGMTCAPRRLHLCNKNPNNNSNDSSKAKHDLAEVCMARKYEGESIK 157
DB 71 QDNNDKKFKTIDSTSDSNNTIDFIYNLPTQNTIN-----QLTK----- 110
QY 158 THYPRYSKYPSGSDPFCMTMLARSP---ADIGIIRGRDLYLGNKKKKONGK----- 206
DB 111 ---NKTDNT-----SLTTLIQNLFNLSNDSIDYEQFRN---GRKSTNDSKNSDNSTKN 159
QY 207 --ETEREKLQKLEIFKFIHDNLKDKKAEQKRYNGD-----DPNFKLREDMTANRET 259
DB 160 DTPQSSKQDKADNQKAPK-SNNTKPSSTSNKQPNSPKPTQPNQSNQPSADD--KANQK- 215
QY 260 VMCAMTCSKELDNSSYFRATCN-----DTGGPQGTANRCKRCDKDKGANAKPKRAGD 311
DB 216 -----SSSKDNQSMDSALDSILDQYSBPAKKTORDVYASQSKDKDKNEKSNNTNQ- 265
QY 312 GDTVTPYFDYVPQYLRFEEWABDFCRKKKKKLENLEKQCRGKD 357
DB 266 -----LPT-----QDELKHKSKFAQSFPNNDVNOKD 290

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Search completed: December 29, 2005, 23:40:22
Job time : 4.64597 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model1

Run on: December 29, 2005, 23:10:51 ; Search time 7.68993 Seconds
(without alignment)
3623.140 Million cell updates/sec

Title: US-09-508-967-1_COPY_79_415
Perfect score: 1884
Sequence: 1 PCKKDGKGNVDKRSVKEQA.....GSYENWIDNOKKQKQKQK 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	892.5	47.4	2182	1 US-08-487-826B-16	Sequence 16, Appl
2	885	47.0	2710	1 US-08-568-459A-12	Sequence 12, Appl
3	885	47.0	2710	1 US-08-487-826B-12	Sequence 12, Appl
4	885	47.0	2710	2 US-09-210-288-12	Sequence 12, Appl
5	885	47.0	2710	2 US-10-153-273-12	Sequence 12, Appl
6	885	47.0	3060	1 US-08-487-826B-14	Sequence 14, Appl
7	845	44.9	700	1 US-08-568-459A-10	Sequence 10, Appl
8	845	44.9	700	1 US-08-487-826B-10	Sequence 10, Appl
9	845	44.9	700	2 US-09-210-288-10	Sequence 10, Appl
10	845	44.9	700	2 US-10-153-273-10	Sequence 10, Appl
11	653	34.7	3542	2 US-10-087-013-2	Sequence 2, Appl
12	379.5	20.1	362	1 US-08-568-459A-18	Sequence 18, Appl
13	379.5	20.1	362	1 US-08-487-826B-18	Sequence 18, Appl
14	379.5	20.1	362	2 US-09-210-288-18	Sequence 18, Appl
15	379.5	20.1	362	2 US-10-153-273-18	Sequence 18, Appl
16	360.5	19.1	411	1 US-08-568-459A-19	Sequence 19, Appl
17	360.5	19.1	411	1 US-08-487-826B-19	Sequence 19, Appl
18	360.5	19.1	411	1 US-09-210-288-19	Sequence 19, Appl
19	360.5	19.1	411	2 US-10-153-273-19	Sequence 19, Appl
20	281	14.9	1435	1 US-08-568-459A-4	Sequence 4, Appl
21	281	14.9	1435	1 US-08-487-826B-4	Sequence 4, Appl
22	281	14.9	1435	2 US-09-210-288-4	Sequence 4, Appl
23	281	14.9	1435	2 US-10-153-273-4	Sequence 4, Appl
24	280.5	14.9	749	1 US-08-568-459A-6	Sequence 6, Appl
25	280.5	14.9	749	1 US-08-487-826B-6	Sequence 6, Appl
26	280.5	14.9	749	2 US-09-210-288-6	Sequence 6, Appl
27	280.5	14.9	749	2 US-10-153-273-6	Sequence 6, Appl

28	241	12.8	921	1 US-08-568-459A-8	Sequence 8, Appl
29	241	12.8	921	1 US-08-487-826B-8	Sequence 8, Appl
30	241	12.8	921	2 US-09-210-288-8	Sequence 8, Appl
31	241	12.8	921	2 US-10-153-273-8	Sequence 8, Appl
32	229.5	11.7	311	2 US-10-087-013-10	Sequence 10, Appl
33	220	11.7	407	2 US-10-087-013-8	Sequence 8, Appl
34	218	11.6	308	2 US-10-087-013-11	Sequence 11, Appl
35	213.5	11.3	351	2 US-10-087-013-9	Sequence 9, Appl
36	207	11.0	1115	1 US-08-568-459A-2	Sequence 2, Appl
37	207	11.0	1115	1 US-08-487-826B-2	Sequence 2, Appl
38	207	11.0	1115	2 US-09-210-288-2	Sequence 2, Appl
39	207	11.0	1115	2 US-10-153-273-2	Sequence 2, Appl
40	207	11.0	1115	6 5198347-6	Patent No. 5198347
41	205	10.9	294	2 US-10-087-013-7	Sequence 7, Appl
42	197.5	10.5	411	1 US-08-568-459A-20	Sequence 20, Appl
43	197.5	10.5	411	1 US-08-487-826B-32	Sequence 32, Appl
44	197.5	10.5	411	2 US-09-210-288-20	Sequence 20, Appl
45	197.5	10.5	411	2 US-10-153-273-20	Sequence 20, Appl

ALIGNMENTS

```

RESULT 1
US-08-487-826B-16
; Sequence 16, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhuan
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-487-826B-16
Query Match 47.4%; Score 892.5; DB 1; Length 2182;

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Best Local Similarity 51.9%; Pred. No. 4,56-75;
Matches 182; Conservative 47; Mismatches 69; Indels 53; Gaps 12;

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QY 1 PCKKDGKNDVDRFS-----YKQAGYNNKKKCKSGNMTCAFPFRRLHLCNNKFP 49
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Db 99 PCRDKAKEDVNRSDTIGGCTTNRICDSQGGNKV-----GACAPYRLHLCDY--- 149
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QY 50 MNSNSKAKHDLAECVMAKYEKESIKTHYPKYDSKYPGSPFPMCTMLARSPADIGD 109
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 150 NLESIDTSTTHKLLEVCMAKYEKESINTHYQRTNEDSASQCLTVLARSFADIGD 209
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 110 IIRGDLVLG--NKKKKONGKETEREKLEKQLEKFKI--DNLDKQAKRYNGD--EDP 165
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 210 IVRGDLVLGYDNKEKEQ-----RKLEQKLEKIDFKIHDVMTKNGAQERYIDDAKG 263
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 166 NPYKLRDMWTANRTEVGMATCSKELDNSSYFRATCNDTGQGSQTHNKRCDKXKAN 225
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 264 DFOUREDMWTSNRTWKALICHAPKANYFIKTACN--VGKQ---TNGQCHC----- 312
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QY 226 AGKPAAGDGVTVTVTFYDYVPQYLRFWEEMAEDECRKKKKLEMLEKQCGKDKSDEYR 285
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Db 313 -----IGGD-----VPTFYDYVPQYLRFWEEMAEDECRKKKKLEMLEKQCGDYEQN---L 360
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QY 286 YCSRNGYCEOTISRKGKVRMGKCTDCFPAGSYENWIDNQRKQFDKQK 336
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 YCSGNGYCTKTYYKKGLVIGEHCTNCSVWCMTYETIDNQKEFLKQKR 411
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```

RESULT 2
US-08-568-459A-12
; Sequence 12, Application US/08568459A
; Patent No. 5849306

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459A
FILING DATE: 07-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO

ORIGINAL SOURCE:

; ORGANISM: Plasmodium falciparum
; US-08-568-459A-12

Query Match 47.0%; Score 885; DA 1; Length 2710;
Best Local Similarity 50.7%; Pred. No. 3,1e-74;
Matches 174; Conservative 46; Mismatches 77; Indels 46; Gaps 10;

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QY 1 PCR-----KDGKNDVDRFSYKQAGYNNKKKCKSGNMTCAFPFRRLHLCNNKFP 53
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Db 91 PCADRSVDRFSDEYGGCTTNRIRKDSQGGNKV-----ACAPYRLHVCNDNLEQIEP 143
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QY 54 NDSKAKHDLAECVMAKYEKESIKTHYPKYDSKYPGSPFPMCTMLARSPADIGIIRG 113
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 144 IKTTNT--HNLVLVVCMAKYEKESITODYIKYATIGDSQSQCLTVLARSFADIGDVRG 202
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 114 RDLVLGKKKKONGKETEREKLEKQLEKFKIHDNLDKQAKRYNGEDPNFYKLRD 173
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 203 RDLVLGKPKQIK-----QROQLNNLKTIFGKIYEKLNGAEA--RYG--NDPEFFKLRED 253
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 174 WMTANRETVMGAMTCSKELDNSSYFRATCNDTGQGSQTHNKRCDKXKANAGKPAAGD 233
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 254 WMTANRETVMKAITCNAM--GNTYFATCN--RG--ERTGYCRDNDQ----- 236
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QY 234 GDTVTYVPTFYDYVPQYLRFWEEMAEDECRKKKKLEMLEKQCGKDKSDEYRCSRNGYD 293
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 -----VPTFYDYVPQYLRFWEEMAEDECRKKKKLEMLEKQCGKDKSDEYRCSRNGYD 351
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 3
US-08-487-826B-12
; Sequence 12, Application US/08487826B
; Patent No. 5993827

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
US-08-487-8268-12

Query Match 47.0%; Score 885; DB 1; Length 2710;
Best Local Similarity 50.7%; Pred. No. 3.1e-74;
Matches 174; Conservative 46; Mismatches 77; Indels 46; Gaps 10;

QY 1 PCK-----KDGKNDVDRFSYKQAGYDNKKKCSNGMTCAFPRLHLCKNFPNNNS 53
DB 91 PCADRSDFRFSDEYGGCTHNRKIDSGQGNKG-----ACAPYRLHVCDDQNLQIEP 143
QY 54 NDSKAKHDLAEVCMAYEGESIKTHYPKYDSKYPGSDPFPMCTMLARSPADIGDIIRG 113
DB 144 IKITNT-HNLIVDCMAAKFEGOSITDYPKYQATYGSPSQICTMLARSPADIGDIVRG 202
QY 114 RDLVGNKKKKQNGKETEREKLEQKKEIFKKIHDLKDKAQRKYNQDDEPNFYKLRD 173
DB 203 RDLVGNFQKIK-----ORQLENNLKITFGKIYEKLGAAEA--RYG--NDPEFKLRD 253
QY 174 WMTANRETVMGAMTCSKELDNSSYFRATCNDTGGSPQTHNKCRCDDKXGKAGNAGKPKXAGD 233
DB 254 WMTANRETVMKAITCTNAM--GNTYFHATCN--RG-ERTKGYCRCNDQD----- 296
QY 234 GDTVIVPTFYDPVPOYLRFMEFEWADFCRKKKKLENEKOCRGKDSDEYRYSRNGYD 293
DB 297 -----VPTFYDPVPOYLRFMEFEWADFCRKKKKIKDYKRNCRGDKDKORYSRNGYD 351
QY 294 CEQTSIRKQKVRMGKCTDCEFFACGSYNNWIDNQRKQPKQK 336
DB 352 CEKTKRAIGKLRYGKQICISLYACNPYVDWNNQKEQFDKQK 394

RESULT 4
US-09-210-288-12
Sequence 12, Application US/09210288
Patent No. 6392026

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
US-09-210-288-12

Query Match 47.0%; Score 885; DB 2; Length 2710;
Best Local Similarity 50.7%; Pred. No. 3.1e-74;
Matches 174; Conservative 46; Mismatches 77; Indels 46; Gaps 10;

QY 1 PCK-----KDGKNDVDRFSYKQAGYDNKKKCSNGMTCAFPRLHLCKNFPNNNS 53
DB 91 PCADRSDFRFSDEYGGCTHNRKIDSGQGNKG-----ACAPYRLHVCDDQNLQIEP 143
QY 54 NDSKAKHDLAEVCMAYEGESIKTHYPKYDSKYPGSDPFPMCTMLARSPADIGDIIRG 113
DB 144 IKITNT-HNLIVDCMAAKFEGOSITDYPKYQATYGSPSQICTMLARSPADIGDIVRG 202
QY 114 RDLVGNKKKKQNGKETEREKLEQKKEIFKKIHDLKDKAQRKYNQDDEPNFYKLRD 173
DB 203 RDLVGNFQKIK-----ORQLENNLKITFGKIYEKLGAAEA--RYG--NDPEFKLRD 253
QY 174 WMTANRETVMGAMTCSKELDNSSYFRATCNDTGGSPQTHNKCRCDDKXGKAGNAGKPKXAGD 233
DB 254 WMTANRETVMKAITCTNAM--GNTYFHATCN--RG-ERTKGYCRCNDQD----- 296
QY 234 GDTVIVPTFYDPVPOYLRFMEFEWADFCRKKKKLENEKOCRGKDSDEYRYSRNGYD 293
DB 297 -----VPTFYDPVPOYLRFMEFEWADFCRKKKKIKDYKRNCRGDKDKORYSRNGYD 351
QY 294 CEQTSIRKQKVRMGKCTDCEFFACGSYNNWIDNQRKQPKQK 336
DB 352 CEKTKRAIGKLRYGKQICISLYACNPYVDWNNQKEQFDKQK 394

RESULT 5

US-10-153-273-12
Sequence 12, Application US/10153273
Patent No. 6962987

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH21.1FMDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-153-273-12

Query Match 47.0%; Score 885; DB 2; Length 2710;
Best Local Similarity 50.7%; Pred. No. 3.1e-74;
Matches 174; Conservative 46; Mismatches 77; Indels 46; Gaps 10;

QY 1 PCK-----KDGKNDVDRFSVKEAGYDNKKKCSNGMTCAPEPRRLHLCNKPNNNS 53
DB 91 PCADRSDFRFSDEYGGQCTHNRIDSGQDNKG-----ACAPRRRLHVCDDNLEQIEP 143
QY 54 NDSSKAKHDLAEVCMAYEGESIKTHYPKYDSKYPGSDPFCMTMLARSPADIGDIIRG 113
DB 144 IKITNT-HNLLVDVCMAYEGESITODYPKYQATYGSPSQICMTMLARSPADIGDIYRG 202
QY 114 RDLVGNKKKKKONGETEREKLEQKLEIKKHIDNLDKKAQKRYNGDEDPNFKLRED 173
DB 203 RDLVGNQOEIK-----QRQLENNLKTIPEGIYEKLNGBA--RYG--NDPEFKLRED 253
QY 174 WMTANRETVMGAMTCSKELDNSSYFRATCNPTGGPSQTHNKCRCDDKGNAGKPKACD 233
DB 254 WMTANRETVMKAITCNAM--GNTYFHATCN--RG-ERTKGYCRNDQO----- 296
QY 234 GDVTIVPTFYDYPQYLRFWEFEMADEFCRKKKKKLENEKOCRGKDSDEYRYSRNGYD 293
DB 297 -----VPTFYDYPQYLRFWEFEMADEFCRKKKKIKDYKRCRGKDXKDRYCSRNGYD 351
QY 294 CEQTSRKGYRMGKCTDCCFPACGSYENWIDNQRKQPKOKK 336
DB 352 CEKTRRAIGKLRYGKQCTISCLYACNPYDWINNKEQFPDKOKK 394

RESULT 6

US-08-487-826B-14
Sequence 14, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelien, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH21.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3060 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-826B-14

Query Match 47.0%; Score 885; DB 1; Length 3060;
Best Local Similarity 50.7%; Pred. No. 3.6e-74;
Matches 174; Conservative 46; Mismatches 77; Indels 46; Gaps 10;

QY 1 PCK-----KDGKNDVDRFSVKEAGYDNKKKCSNGMTCAPEPRRLHLCNKPNNNS 53
DB 89 PCADRSDFRFSDEYGGQCTHNRIDSGQDNKG-----ACAPRRRLHVCDDNLEQIEP 141
QY 54 NDSSKAKHDLAEVCMAYEGESIKTHYPKYDSKYPGSDPFCMTMLARSPADIGDIIRG 113
DB 142 IKITNT-HNLLVDVCMAYEGESITODYPKYQATYGSPSQICMTMLARSPADIGDIYRG 200
QY 114 RDLVGNKKKKKONGETEREKLEQKLEIKKHIDNLDKKAQKRYNGDEDPNFKLRED 173
DB 201 RDLVGNQOEIK-----QRQLENNLKTIPEGIYEKLNGBA--RYG--NDPEFKLRED 251
QY 174 WMTANRETVMGAMTCSKELDNSSYFRATCNPTGGPSQTHNKCRCDDKGNAGKPKACD 233
DB 252 WMTANRETVMKAITCNAM--GNTYFHATCN--RG-ERTKGYCRNDQO----- 294
QY 234 GDVTIVPTFYDYPQYLRFWEFEMADEFCRKKKKKLENEKOCRGKDSDEYRYSRNGYD 293
DB 295 -----VPTFYDYPQYLRFWEFEMADEFCRKKKKIKDYKRCRGKDXKDRYCSRNGYD 349
QY 294 CEQTSRKGYRMGKCTDCCFPACGSYENWIDNQRKQPKOKK 336
DB 350 CEKTRRAIGKLRYGKQCTISCLYACNPYDWINNKEQFPDKOKK 392

RESULT 7

US-08-568-459A-10
Sequence 10, Application US/08568459A
Patent No. 5849306
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California

```

; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,459A
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelien, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; US-08-568-459A-10

```

Query Match 44.9%; Score 845; DB 1; Length 700;

Best Local Similarity 54.9%; Pred. No. 3e-71;

Matches 168; Conservative 43; Mismatches 59; Indels 36; Gaps 10;

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QY 35 CAPPRRLHLCKNPPNNSNDSSAKADLAELVCAAKYEGESJIKTHPKYDSKYPGSD 94
DB 10 CAPPRRLHLCY---NLESIDTSTHKLLEVCMAAYEGENSINTHYTORHTEBDSAS 66
QY 95 PMCTMLARSPADIDGDIIRGDLVYG--NKKKKONGKTEREKLEOKLEIKKIH-DNLK 151
DB 67 QLCVTLARSPADIDGDIIRGDLVYGDKKEQ-----RKKLEOKKDIKFIKHKDVMK 120
QY 152 DKEAKRYNGD-EDPNFYKLREDMTANRETVMGAMTCSKELDNSSYFRATCNDTGOGPS 210
DB 121 TNGAQRITIDAKGDFPQLREDMTSNRETVMKALICHAPKEANYFIKTACN-VGKG-- 177
QY 211 QTHNKCRCDDKDGANAGKPKAGDGVITVPTYPDYVPQYLRFEMWADFCRKKKKKLEN 270
DB 178 -TNGQCHC-----IGD-----VPTYPDYVPQYLRFEMWADFCRKKKKKLEN 220
QY 271 LEKCRGKDSDEYRYCSRNGYCEQITSRKGVRMGKGTDCFPACGSYENWIDNQRKQ 330
DB 221 LQKCRDYEON---LYCSGNGYDCTKTIYKKGKLVIGSHCTNCSVWCMEYETWIDNQRKE 277
QY 331 FDKOKK 336
DB 278 FLKQKR 283

```

RESULT 8

US-08-487-826B-10

; Sequence 10, Application US/08487826B

; Patent No. 5993827

; GENERAL INFORMATION:

; APPLICANT: Sim, Kim L.

; APPLICANT: Chitnis, Chetan

; APPLICANT: Miller, Louis H.

; APPLICANT: Peterson, David S.

; APPLICANT: Su, Xin-zhaun

; APPLICANT: Willems, Thomas E.

; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

; NUMBER OF SEQUENCES: 45

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelien, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
; US-08-487-826B-10

```

Query Match 44.9%; Score 845; DB 1; Length 700;

Best Local Similarity 54.9%; Pred. No. 3e-71;

Matches 168; Conservative 43; Mismatches 59; Indels 36; Gaps 10;

```

QY 35 CAPPRRLHLCKNPPNNSNDSSAKADLAELVCAAKYEGESJIKTHPKYDSKYPGSD 94
DB 10 CAPPRRLHLCY---NLESIDTSTHKLLEVCMAAYEGENSINTHYTORHTEBDSAS 66
QY 95 PMCTMLARSPADIDGDIIRGDLVYG--NKKKKONGKTEREKLEOKLEIKKIH-DNLK 151
DB 67 QLCVTLARSPADIDGDIIRGDLVYGDKKEQ-----RKKLEOKKDIKFIKHKDVMK 120
QY 152 DKEAKRYNGD-EDPNFYKLREDMTANRETVMGAMTCSKELDNSSYFRATCNDTGOGPS 210
DB 121 TNGAQRITIDAKGDFPQLREDMTSNRETVMKALICHAPKEANYFIKTACN-VGKG-- 177
QY 211 QTHNKCRCDDKDGANAGKPKAGDGVITVPTYPDYVPQYLRFEMWADFCRKKKKKLEN 270
DB 178 -TNGQCHC-----IGD-----VPTYPDYVPQYLRFEMWADFCRKKKKKLEN 220
QY 271 LEKCRGKDSDEYRYCSRNGYCEQITSRKGVRMGKGTDCFPACGSYENWIDNQRKQ 330
DB 221 LQKCRDYEON---LYCSGNGYDCTKTIYKKGKLVIGSHCTNCSVWCMEYETWIDNQRKE 277
QY 331 FDKOKK 336
DB 278 FLKQKR 283

```

RESULT 9

US-09-210-288-10

; Sequence 10, Application US/09210288

; Patent No. 6392026

; GENERAL INFORMATION:

; APPLICANT: Sim, Kim L.

; APPLICANT: Chitnis, Chetan

; APPLICANT: Miller, Louis H.

; APPLICANT: Peterson, David S.

```

1  APPLICANT: Su, Xin-zhaun
2  APPLICANT: Wellems, Thomas B.
3  TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
4  TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
5  NUMBER OF SEQUENCES: 37
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Knobbe Martens Olsson & Bear
8  STREET: 620 Newport Center Drive 16th Floor
9  CITY: Newport Beach
10 STATE: California
11 COUNTRY: US
12 ZIP: 92660
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/210,288
20 FILING DATE:
21 CLASSIFICATION:
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Fuller, Michael
24 REGISTRATION NUMBER: 36,516
25 REFERENCE/DOCKET NUMBER: NIH21.1FMDV1
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (619) 235-8550
28 TELEFAX: (619) 235-0176
29 INFORMATION FOR SEQ ID NO: 10:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 700 amino acids
32 TYPE: amino acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 MOLECULE TYPE: protein
36 HYPOTHETICAL: NO
37 ORIGINAL SOURCE:
38 ORGANISM: Plasmodium falciparum
39 JS-09-210-288-10

```

Query Match	44.9%	Score 845	DB 21	Length 700
Best Local Similarity	54.9%	Pred. No. 3e-71		
Matches 168	Conservative 43	Mismatches 55	Indels 36	Gaps 10
QY	35	CAPERRRLCTCKNFPNNMNSNDSSKAKHDLLEVCMAAYKEBSIKTHYKDYSKYSGSDF	94	
Db	10	CAPRRRLHLCGY---NLESIDTTSPTHTLLLEVCMAAYKEBSINTHTYGTQRTVEDSAS	66	
QY	95	PMCTMLARSPADIGIITIRGRDLYL--NKKKKQNGKETEREKLKELKRIKTH--DNLK	151	
Db	67	QLCTVLAASFADIGIIVRGKDLTYGYDMKEKQ-----RKLEQKLDIFKKIKHDKVMK	120	

QY	152	DKEADKRNKG-D	EDNPFYLREDWMTANETWGAATCSKEIDNSSYPFATCDTGOGS	210
Db	121	TNGAERIIIDAKGSD	FQLREDWMTSNRETYMKLICHAPKEANFITRACH-VGR--	177
QY	211	QTNRKCRDCKGANAGRP	KAGDGDTIVTPYFDVYPOYLRFMEEAEDFCRRKKKLTEN	270
Db	178	-TNGCHC-----	IGGD-----VPYFDVYPOYLRFMEEAEDFCRRKKKLTEN	220
QY	271	LEKCRGDKDSERYICSHNGYDCB	OTIRSKRVNRKGCCTDFCFACGSYEAMIDNQRO	330
Db	221	LQKCRDEYN---	LYCSGNGYDCTKTITVKKGLVIGEHCTWCSCRMETWIDNQKE	277
QY	331	FDKOKK	336	
Db	278	FLKOKR	283	

RESULT 10
US-10-153-273-10
; Sequence 10, Application US/10153273
; Patent No. 6962987

```

1  GENERAL INFORMATION:
2  APPLICANT: Sim, Kim L.
3      Chitnis, Chetan
4      Miller, Louis H.
5      Peterson, David S.
6      Su, Xin-zhaun
7      Wellem, Thomas E.
8  TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
9      AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
10
11  NUMBER OF SEQUENCES: 37
12  CORRESPONDENCE ADDRESS:
13      ADDRESSEE: Knobbe Martens Olson & Bear
14      STREET: 620 Newport Center Drive 16th Floor
15      CITY: Newport Beach
16      STATE: California
17      COUNTRY: US
18      ZIP: 92660
19
20  COMPUTER READABLE FORM:
21      MEDIUM TYPE: Floppy disk
22      COMPUTER: IBM PC compatible
23      OPERATING SYSTEM: PC-DOS/MS-DOS
24      SOFTWARE: Patentin Release #1.0, Version #1.25
25
26  CURRENT APPLICATION DATA:
27      APPLICATION NUMBER: US/10/153,273
28      FILING DATE: 21-May-2002
29      CLASSIFICATION: <Unknown>
30
31  PRIOR APPLICATION DATA:
32      APPLICATION NUMBER: US/09/210,288
33      FILING DATE: <Unknown>
34
35  ATTORNEY/AGENT INFORMATION:
36      NAME: Fuller, Michael
37      REGISTRATION NUMBER: 36,516
38      REFERENCE/DOCKET NUMBER: NIH21.1FMDV1
39  TELECOMMUNICATION INFORMATION:
40      TELEPHONE: (619) 235-8550
41      TELEFAX: (619) 235-0176
42
43  INFORMATION FOR SEQ ID NO: 10:
44      SEQUENCE CHARACTERISTICS:
45          LENGTH: 700 amino acids
46          TYPE: amino acid
47          STRANDEDNESS: single
48          TOPOLOGY: linear
49      MOLECULE TYPE: protein
50      HYPOTHEetical: NO
51      ORIGINAL SOURCE:
52          ORGANISM: Plasmodium falciparum
53      SEQUENCE DESCRIPTION: SEQ ID NO: 10:
54      US-10-153-273-10

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Query Match	44.9%	Score 845; DB 2;	Length 700;
Best Local Similarity	54.9%	Pred. No. 3e-71;	
Matches 168; Conservative	43;	Mismatches 59;	Indels 36; Gaps 10;

Qy	35	CAPEPRRLHLCNKNFENPMNMSNDSSKKKHDLLEAVCNAAKYEGESIKTHYEPKYDSKYPGSDF	94
Db	10	CAPPRRLHLCGY---NLIESIDTSTTHKLLLEVCNAAKYEGNSINTHYHQRTMEDSAS	66
Qy	95	PMCMTLARSPADIDGIIIRGRDLYG--NKKKKRONKETERELBOKIKXIPEKIH--DNLK	151
Db	67	QCLTVLASFADIGIYVNGKDIYLYADNNEKQ-----RKLRLBKXNDIPEKIHDDVWK	120
Qy	152	DKEAQKRYNGD-EDPNFYKLEEDMWTANRETJVGMATCSKELDNSSYFATCNDTGOQGS	210
Db	121	TNGAQERYIDDAKAGDFFQRLREDMWTSNRETIWKALICHAPKEANYFITACN-VQKG--	177
Qy	211	QTHHKCRDNDKGNAGAKPKAGDGDVTLVPTFYFDVPOYLRFYFEEMADFCRKKKKKLEN	270
Db	178	TNQGCHC-----IGSD-----VPTFYFDVPOYLRFYFEEMADFCRKKKKKLEN	220
Qy	271	LEKQCRGKDSDEYRYCSRNGYDEQIITSRKGKVMGKGCCTDCCFPAQSGSYENWIDNQKQ	330
Db	221	LQKQCRDNDV---LYCGSNGYDCKITLYKKGKLVIGHCNTGCSWCRARYETWIDNQKE	277

[illegible]

Qy 331 FDXOKK 336
Db 278 FLKOKR 283

RESULT 11

US-10-087-013-2
Sequence 2, Application US/10087013
Patent No. 6855323
GENERAL INFORMATION:
APPLICANT: Arthur Scherf
APPLICANT: Louis H. Miller
APPLICANT: Benoit Gamain
APPLICANT: Doro I. Barnuch
APPLICANT: Pierre Buffet
APPLICANT: Christine Scheidig
APPLICANT: Bruno Pouvelle
APPLICANT: Joseph Smith
APPLICANT: No. 6855323utaka Fujii
TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
FILE REFERENCE: NIH176.001C1
CURRENT APPLICATION NUMBER: US/10/087,013
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: PCT/US00/24195
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/152,023
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 3542
TYPE: PRT
ORGANISM: Plasmodium falciparum
US-10-087-013-2

Query Match 34.7%; Score 653; DB 2; Length 3542;

Best Local Similarity 40.9%; Pred. No. 4.1e-52;
Matches 147; Conservative 48; Mismatches 100; Indels 64; Gaps 15;

Qy 1 PCKKDKG-----GNDVRSVKEQAGYDNK---KMKSGNGTCAEFR 39
Db 87 PCNLDHKEHTNLRQDVNLRHPCRGQRBNRFDDEDESCGNKIRYKAK-NDALACAPPR 145
Qy 40 RLHLCKNCFPMNNSNDSSKAKGDLAEVCMAYEGESIKTHYPKYDSKYPGSDPFMCTM 99
Db 146 RRMHCDKNLEALNINTQNT-HDLLGNLVYAKTEGESIVNNHP-----HKGTG-DACTA 198
Qy 100 LARSFADIGDIIRGRDLYLGNKKKKKQNGKETEREKLEQKLKEIFKIHDLKDXEAQKRY 159
Db 199 LARSFADIGDIVRGIDMF-----KPVVHDVETGLREVFVKIHDMED-EVKNXY 247
Qy 160 NGDDDPNRYKLRBDMWTANRETWGAMTCSKELDNSSYFRATCNDTGGPSQTHNKKCD 219
Db 248 NPDSGNTYKLRBDMWTANRETWGAMTCSKELDNSSYFRATCNDTGGPSQTHNKKCD 300
Qy 220 KDKGANAGKPYAGDGVTVIVTFYFDVYPOYLRFEEWAEDFCRKKKKLEMLEKQCRGKD 279
Db 301 ---GHKQK-----VPTNLDYVPOYLRWPEWEEFCRKNKIKLKVKYKQSCR-ND 346
Qy 280 KSDERYYSRNGYDCEQITSRKGVKMGKCTDCCFACGSYEMWIDNQRQPFQKQ-KY 337
Db 347 K-ERLYCSHNGHDCITTIWKKGILHLNDKCTDCSTCKVFEVWLGNOQBAFKQKQKXY 403

RESULT 12

US-08-568-459A-18
Sequence 18, Application US/08568459A
Patent No. 5849306
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: WeiJiems, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe Martens Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: California

COUNTRY: US

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/568,459A

FILING DATE: 07-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Israelien, Ned

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH121.001CP1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-0176

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 362 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

US-08-568-459A-18

Query Match 20.1%; Score 379.5; DB 1; Length 362;

Best Local Similarity 31.3%; Pred. No. 1.5e-27;
Matches 93; Conservative 14; Mismatches 149; Indels 41; Gaps 5;

Qy 35 CAPPRRLHLCKNCFPMNNSNDSSKAKGDLAEVCMAYEGESIKTHYPKYDSKYPGSDPF 94
Db 2 CAPPRRLHLCDY--NLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 58
Qy 95 PMCTMLARSFADIGDIIRGRDLYG--NKKKKQNGKETEREKLEQKLKEIFKIHDLKDX 152
Db 59 QLCVTLARSFADIGDIVRGKOLYGYDNKXXXXXXXXXXXXXXXXXXXXXXXXXXXX 118
Qy 153 KEAQKRNGBDEPFYKLRBDMWTANRETWGAMTCSKELDNSSYFRATCNDTGGPSQT 212
Db 119 XXXXXXXXGGD---FQLRBDMWTANRETWGAMTCSKELDNSSYFRATCNDTGGPSQT 164
Qy 213 HNKCRCDKGANAGKPYAGDGVTVIVTFYFDVYPOYLRFEEWAEDFCRKKKKLEMLE 272
Db 165 -----XXXXXXXXXXXXXXXXXXXXXXXXXXVPOYLRWPEWEEFCRKKKKLEMLE 214
Qy 273 KQCRGKDKSDERYYSRNGYDCEQITSRKGVKMGKCTDCCFACGSYEMWIDNQRK 329
Db 215 KQ-----CXXXXXXXXXXXXXXXXXXXXCTNCSVWCRMYETWIDNQK 259

RESULT 13

US-08-487-826B-30
Sequence 30, Application US/08487826B
Patent No. 5993827

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; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; NUMBER OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-487-826B-30

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Query Match 20.1%; Score 379.5; DB 1; Length 362;
Best Local Similarity 31.3%; Pred. No. 1.5e-27;
Matches 93; Conservative 14; Mismatches 149; Indels 41; Gaps 5;

QY 35 CAPPRRLHLCKNKPNNMNSDSKAKHDLAEVCMARYEGESIKTHYPKYDSKYPGSDF 94
DB 2 CAPPRRLHLCDY--NLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 58
QY 95 PMCTMLARSPADIDIGIRGDLVIG--NKKKKQNGKETEREKLEQKLEIFKIHDLNLD 152
DB 59 QLCIVLARSPADIDIGIRGDLVIGYDNKXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 118
QY 153 KEAQKRYNGEDDPNYFLKREDMTANRETYWGAMTCSKELDNSYFPATCNIDTGOGPGQT 212
DB 119 XXXXXXXKGD---FPQLREDMTSNRETWKALICHAXXXXXXXXXXXXXC----- 164
QY 213 HNKRCCKDKGANGKPRAGDGVITVPTVFDYVPOYLRFEEWAEDFCRKKKKLENTLQ 272
DB 165 -----XXXXXXXXXXXXXXXXXXXXXXXXXXXXVPOYLRFEEWAEDFCRKKKKLENTLQ 214
QY 273 KQCRGKDSDEYRCSRNGYDCEQGTISRKGVRMGKCTDGFACGSYENNIQNRK 329
DB 215 KQ-----CXXXXXXXXXXXXXXXXXXXXXCTNCSVWCMTETWIDNQK 259

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RESULT 14
US-09-210-288-18

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; Sequence 18, Application US/09210288
; Patent No. 6392026
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; NUMBER OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-09-210-288-18

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Query Match 20.1%; Score 379.5; DB 2; Length 362;
Best Local Similarity 31.3%; Pred. No. 1.5e-27;
Matches 93; Conservative 14; Mismatches 149; Indels 41; Gaps 5;

QY 35 CAPPRRLHLCKNKPNNMNSDSKAKHDLAEVCMARYEGESIKTHYPKYDSKYPGSDF 94
DB 2 CAPPRRLHLCDY--NLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 58
QY 95 PMCTMLARSPADIDIGIRGDLVIG--NKKKKQNGKETEREKLEQKLEIFKIHDLNLD 152
DB 59 QLCIVLARSPADIDIGIRGDLVIGYDNKXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 118
QY 153 KEAQKRYNGEDDPNYFLKREDMTANRETYWGAMTCSKELDNSYFPATCNIDTGOGPGQT 212
DB 119 XXXXXXXKGD---FPQLREDMTSNRETWKALICHAXXXXXXXXXXXXXC----- 164
QY 213 HNKRCCKDKGANGKPRAGDGVITVPTVFDYVPOYLRFEEWAEDFCRKKKKLENTLQ 272
DB 165 -----XXXXXXXXXXXXXXXXXXXXXXXXXXXXVPOYLRFEEWAEDFCRKKKKLENTLQ 214
QY 273 KQCRGKDSDEYRCSRNGYDCEQGTISRKGVRMGKCTDGFACGSYENNIQNRK 329
DB 215 KQ-----CXXXXXXXXXXXXXXXXXXXXXCTNCSVWCMTETWIDNQK 259

```

RESULT 15
US-10-153-273-18
Sequence 18, Application US/10153273
Patent No. 6962987
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
Chilnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Knodbe Martens Olsson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FMDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-153-273-18
Query Match 20.1%; Score 379.5; DB 2; Length 362;
Best Local Similarity 31.3%; Pred. No. 1.5e-27;
Matches 93; Conservative 14; Mismatches 149; Indels 41; Gaps 5;
QY 35 CAPPRRLHLCNKNPNNMNSDSKAKHDLAEVCAAYEGESITKHYPKYDSKYPGSGDF 94
DB 2 CAPPRRLHLCY---NLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 58
QY 95 PMCTMLARSPADIGDIIRGDLVIG--NKKKKQNGKETEREKLEQKLEIFRKIHDLKID 152
DB 59 QLCITLARSFADIGIYRGKDLVIGYDNKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 118
QY 153 KEAQRYNGDEDPNFKREDMTANRETWGAATCSKELDNSYFRATCNIDTGGPSQT 212
DB 119 XXXXXXXKGD---FPQLRBDPMWTSNRETVMALICHAXXXXXXXXXXXXC----- 164
QY 213 HNKGRCDKDGANGKPKAGDGVITVPTVDFYVPOYLRFWEWADEFCRKKKKLENTLE 272
DB 165 -----XXXXXXXXXXXXXXXXXXXXXVPQYLRFWEWADEFCRKKKKLENTLQ 214

QY 273 KQCKGKDSDEYRYCSHNGYDCBQTTSRKGVKMGKCTDPCFACSGSYENWIDNQK 329
DB 215 KQ-----CXXXXXXXXXXXXXXXXXXXXXXXXCTNCSVCRMYETWIDNQK 259

Search completed: December 29, 2005, 23:17:20
Job time : 8.68993 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 23:15:07 ; Search time 36.7534 Seconds
(without alignments)
3831.174 Million cell updates/sec

Title: US-09-508-967-1_COPY_79_415

Perfect score: 1884

Sequence: 1 PCKKDKGKNDVDRFSVKEQA.....GSYENWIDNQRKQPKQKKY 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	885	47.0	2710	4 US-10-153-273-12	Sequence 12, Appl
2	845	44.9	700	4 US-10-153-273-10	Sequence 10, Appl
3	653	34.7	3542	4 US-10-087-013-2	Sequence 2, Appl
4	378.5	20.1	362	4 US-10-153-273-18	Sequence 18, Appl
5	360.5	19.1	411	4 US-10-153-273-19	Sequence 19, Appl
6	308.5	16.4	1143	4 US-09-924-154-14	Sequence 14, Appl
7	308.5	16.4	1210	5 US-10-677-980-2	Sequence 2, Appl
8	281	14.9	1435	4 US-10-153-273-4	Sequence 4, Appl
9	280.5	14.9	749	4 US-10-153-273-6	Sequence 6, Appl
10	280.5	14.9	1086	3 US-09-924-154-15	Sequence 15, Appl
11	270	14.3	616	4 US-10-293-913A-4	Sequence 4, Appl
12	269	14.3	616	4 US-10-293-913A-2	Sequence 2, Appl
13	269	14.3	1421	3 US-09-924-154-13	Sequence 13, Appl
14	241	12.8	921	4 US-10-153-273-8	Sequence 8, Appl
15	235	12.5	972	3 US-09-924-154-16	Sequence 16, Appl
16	228.5	12.2	311	4 US-10-087-013-10	Sequence 10, Appl
17	220	11.7	407	4 US-10-087-013-8	Sequence 8, Appl
18	218	11.6	308	4 US-10-087-013-11	Sequence 11, Appl
19	216.5	11.5	1501	3 US-09-924-154-17	Sequence 17, Appl
20	216.5	11.5	1568	5 US-10-712-533A-12	Sequence 12, Appl
21	213.5	11.3	351	4 US-10-087-013-9	Sequence 9, Appl
22	207	11.0	1115	4 US-10-153-273-2	Sequence 2, Appl
23	205	10.9	294	4 US-10-087-013-7	Sequence 7, Appl
24	197.5	10.5	411	4 US-10-153-273-20	Sequence 20, Appl
25	159.5	8.5	282	4 US-10-153-273-16	Sequence 16, Appl
26	158.5	8.4	277	4 US-10-153-273-15	Sequence 15, Appl
27	128.5	6.8	448	4 US-10-153-668-370	Sequence 370, Appl

28	126	6.7	291	4 US-10-153-273-13	Sequence 13, Appl
29	121	6.4	311	4 US-10-153-273-21	Sequence 21, Appl
30	117.5	6.2	754	4 US-10-153-668-254	Sequence 254, Appl
31	116	6.2	737	5 US-10-450-763-40642	Sequence 40642, A
32	115.5	6.1	281	4 US-10-424-599-145507	Sequence 145507, A
33	115	6.1	324	4 US-10-153-273-17	Sequence 17, Appl
34	111	5.9	1255	5 US-10-471-934-4	Sequence 4, Appl
35	111	5.9	1257	4 US-10-408-765A-1486	Sequence 1486, Ap
36	110.5	5.9	6761	5 US-10-732-923-15035	Sequence 15035, A
37	108	5.7	665	3 US-09-820-843A-107	Sequence 107, App
38	108	5.7	1647	5 US-10-732-923-8314	Sequence 8314, App
39	107.5	5.7	680	6 US-11-097-143-30936	Sequence 30936, A
40	107.5	5.7	870	5 US-10-450-763-30674	Sequence 30674, A
41	107.5	5.7	1064	4 US-10-220-510-1	Sequence 1, Appl
42	107.5	5.7	1064	5 US-10-723-860-3242	Sequence 3242, Ap
43	107	5.7	284	4 US-10-424-599-144189	Sequence 144189, i
44	106.5	5.7	1002	4 US-10-654-416-4	Sequence 4, Appl
45	105	5.6	1154	3 US-09-962-854A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-10-153-273-12
; Sequence 12, Application US/10153273
; Publication No. US20020169305A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; Chitnis, Chetan
; Miller, Louis H.
; Peterson, David S.
; Su, Xin-zhuan
; Williams, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobb Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,273
; FILING DATE: 21-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,288
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum

SEQUENCE DESCRIPTION: SEQ ID NO: 12;
US-10-153-273-12

Query Match 47.0%; Score 885; DB 4; Length 2710;
Best Local Similarity 50.7%; Pred. No. 1.8e-67;
Matches 174; Conservative 46; Mismatches 77; Indels 46; Gaps 10;

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DB 91 PCABRSVDRFSDEYGGQCTHNRKIDSGQDNKG-----ACAFPRRLHVCDDQMLEQIEP 143
OY 54 NDSKAKKDLAEVCMAAKYGESIKTHYPKYDSKYPSSDFPMCTMLARSPADIGDITRG 113
DB 144 IKITWT-HNLVYVCMAAKFBQSITQDYPRYQATYGPSQICTMRLARSPADIGDIYRG 202
OY 114 RDLVYGNFKKKONGKETEREKLEQKLEIFKKIHNLKDKBAOKRYNDEDPNIFYKURED 173
DB 203 RDLVYGNFKKKONGKETEREKLEQKLEIFKKIHNLKDKBAOKRYNDEDPNIFYKURED 253
OY 174 WMTANRETVGMATCSKELDNSSYFRATCNDTGGQPSQTHNKKCRCDKXGKAGNAGKPKAGD 233
DB 254 WMTANRETVGMATCSKELDNSSYFRATCNDTGGQPSQTHNKKCRCDKXGKAGNAGKPKAGD 296
OY 234 GDVTIVFYFVYVPOYLRMFEBMADFCRKKKKKLENIKKOGRGKSDERYRSGRYD 293
DB 297 -----VPTFYFVYVPOYLRMFEBMADFCRKKKKKLENIKKOGRGKSDERYRSGRYD 351
OY 294 CEQTSRKGVKRMGKCTDCFPAGCSYENWIDNOKKOPDKOKK 336
DB 352 CEKTRAIKGLRYGKQCTSLYACNPIYVWIDNOKKOPDKOKK 394
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RESULT 2

US-10-153-273-10
Sequence 10, Application US/10153273
Publication No. US20020169305A1

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

Chilnise, Chetan

Miller, Louis H.

Peterson, David S.

Su, Xin-zhaun

Wellens, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knodde Martens Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: California

COUNTRY: US

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/153,273

FILING DATE: 21-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/210,288

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Fuller, Michael

REGISTRATION NUMBER: 36,516

REFERENCE/DOCKET NUMBER: NIH21.1FMDV1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 700 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Plasmodium falciparum

SEQUENCE DESCRIPTION: SEQ ID NO: 10;

US-10-153-273-10

Query Match 44.9%; Score 845; DB 4; Length 700;
Best Local Similarity 54.9%; Pred. No. 1e-64;
Matches 168; Conservative 43; Mismatches 59; Indels 36; Gaps 10;

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OY 35 CAPPRRLHLCNKNFPMNNSNDSKAKKDLAEVCMAAKYGESIKTHYPKYDSKYPSSDF 94
DB 10 CAPPRRLHLCDY---NLSIDITSTTKLLLEVCMAAKYGNISINTYTOHRTNEDSAS 66
OY 95 PMCTMLARSPADIGDITRGDLYLG--NKKKONGKETEREKLEQKLEIFKKIH-DNLK 151
DB 67 QCTVLARSPADIGDIYRGKDLVGYDNKEQ-----RKLEQKLDIFKKIHKOVMK 120
OY 152 DKAOKRYNGD-EDPNIFYKUREDMWTANRETVGMATCSKELDNSSYFRATCNDTGGQPS 210
DB 121 TNGAERYIDDAKAGDFOLREDMTSNRETVGMATCSKELDNSSYFRATCNDTGGQPS 177
OY 211 QTHNKKCRCDKXGKAGNAGKPKAGDGDVTIVPTFYFVYVPOYLRMFEBMADFCRKKKKLENI 270
DB 178 -TNGQCHC-----IGGD-----VPTFYFVYVPOYLRMFEBMADFCRKKKKLENI 220
OY 271 LEKQGRGKSDERYRSGRYDCEQTSRKGVKRMGKCTDCFPAGCSYENWIDNOKKOPDKOKK 330
DB 221 LQKGRDYEQN---LYSGNGYDCTKTIYKKGLVIEHCTGCSVCMRYETWIDNOKKE 277
OY 331 FDKOKK 336
DB 278 FLKOKR 283
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RESULT 3

US-10-087-013-2
Sequence 2, Application US/10087013
Publication No. US20040062769A1

GENERAL INFORMATION:

APPLICANT: Arthur Scherf

Louis H. Miller

Benolt Gamain

Dior I. Baruch

Pierre Buffet

Christine Scheidig

Jurg Gysin

Bruno Pouvelle

Joseph Smith

APPLICANT: No. US20040062769A1utaka Fujii

TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF

PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1

TITLE OF INVENTION: (PREFM) THAT MEDIATES ADHESION TO CHONDROITIN SULFATE A

FILE REFERENCE: NIH176.001C1

CURRENT APPLICATION NUMBER: US/10/087,013

PRIOR FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: PCT/US00/24195

PRIOR FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: 60/152,023

PRIOR FILING DATE: 1999-09-01

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 3542

TYPE: PRT

ORGANISM: Plasmodium falciparum

US-10-087-013-2

Query Match 34.7%; Score 653; DB 4; Length 3542;
 Best Local Similarity 40.9%; Pred. No. 4.2e-47;
 Matches 147; Conservative 48; Mismatches 100; Indels 64; Gaps 15;

QY 1 PCKDKGK-----GNDVDRFSYKQAGYDNK---KMKCSNGMTCAFR 39
 DB PCNDHKHTMLRYDVNLRRHCHREQRNRFDEDESECGNKIRYKXK-NDALACAPR 145
 QY 40 RLHLCKNCPNNNSNDSSKAKHDLAEVCMATYEGESI KTHYPKYSKTPGSDPFMC 99
 DB 146 RRMHCDKLEALNDINTONI-HDLGNVLYVAKYEGESI VNNHP-----HGTS-DACTA 198
 QY 100 LARSFADIGDIIRGDLVLGKCKKQKQKQKETERELBQKLEIFKIHDLKDXAQGRY 159
 DB 199 LARSFADIGDIIRGIDMF-----KPNVHDYVETGLRBFVKIHDGMD-BVKNDY 247
 QY 160 NGDEDPNFKLREDMTANRETVMGAMTCSKELDNSSYFRATCNDTGQSPGOTHNKCRD 219
 DB 248 NPDSGNVYKLRBAMNVRNKKVMEALITCDASY-KSGYFMQSEST---PLFSNPKC--- 300
 QY 220 KDKGNAKGPAGDGDVTVPTYPYVPOYLRFPEEAMADPCRRKKKKLEMLEKCRGKD 279
 DB 301 ---GHKQCK-----VPTNLDYVPOYLRFPEEAMADPCRRKKKKLEMLEKCRGKD 346
 QY 280 KSDERYRCSRGYDCEQITSRKGRMGKGTDCFPAGSYENWIDNRKQFQK-KY 337
 DB 347 K--RLYCSHNGHDCITTIWKKGILHLNCKTCDSTCKKVPFWLGNQDEAPKQKERY 403

RESULT 4

US-10-153-273-18
 ; Sequence 18, Application US/10153273
 ; Publication No. US20020169305A1
 ; GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

Chitnis, Chetan

Miller, Louis H.

Peterson, David S.

Su, Xin-zhaun

Wellens, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe Martens Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: California

COUNTRY: US

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/153,273

FILING DATE: 21-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/210,288

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Fuller, Michael

REGISTRATION NUMBER: 36,516

REFERENCE/DOCKET NUMBER: NIH121.1FWDV1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 362 amino acids

TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-10-153-273-18

Query Match 20.1%; Score 379.5; DB 4; Length 362;
 Best Local Similarity 31.3%; Pred. No. 1.7e-24;
 Matches 93; Conservative 14; Mismatches 149; Indels 41; Gaps 5;

QY 35 CAPRRRLHLCKNCPNNNSNDSSKAKHDLAEVCMATYEGESI KTHYPKYSKTPGSD 94
 DB 2 CAPRRRLHLCY---NLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 58
 QY 95 PCTMLARSFADIGDIIRGDLVYG--NKKKQKQKETERELBQKLEIFKIHDLKMD 152
 DB 59 QLCVTLARSFADIGDIYRGKDLVYGDKKXXXXXXXXXXXXXXXXXXXXXXXXXXXX 118
 QY 153 KEAQKRYNGDEDPNFKLREDMTANRETVMGAMTCSKELDNSSYFRATCNDTGQSPQT 212
 DB 119 XXXXXXXGQD---FQGLREDMWTSNRETVMKALICHXXXXXXXXXXXXX----- 164
 QY 213 HMKRCDDKCANAKGPAGDGDVTVPTYPYVPOYLRFPEEAMADPCRRKKKKLEMLE 272
 DB 165 -----XXXXXXXXXXXXXXXXXXXXXXXXXXXXVPOYLRFPEEAMADPCRRKKKKLEMLE 214
 QY 273 KCRGKDKSDERYRCSRGYDCEQITSRKGRMGKGTDCFPAGSYENWIDNRKQFQK 329
 DB 215 KQ-----CXKXXXXCXXXXXXXXXXXXXXXXXXXXCTNCSVCMETIWDNRK 259

RESULT 5

US-10-153-273-19
 ; Sequence 19, Application US/10153273
 ; Publication No. US20020169305A1
 ; GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

Chitnis, Chetan

Miller, Louis H.

Peterson, David S.

Su, Xin-zhaun

Wellens, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe Martens Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: California

COUNTRY: US

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/153,273

FILING DATE: 21-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/210,288

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Fuller, Michael

REGISTRATION NUMBER: 36,516

REFERENCE/DOCKET NUMBER: NIH121.1FWDV1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 411 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHEetical: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-10-153-273-19

Query Match 19.1%; Score 360.5; DB 4; Length 411;
 Best Local Similarity 29.1%; Pred. No. 9,3e-23;
 Matches 86; Conservative 22; Mismatches 155; Indels 33; Gaps 5;

QY 35 CAPFRRLCNKNFNNMNSDSKAKHDLAEVCAAAAYEGESIKTHYPKYDSKYPGSDF 94
 |||:||||:|
 DB 34 CAPYRLHVCDQNL-XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 92
 QY 95 PMCTMLASFADIGDIIRGRDLYLGNKKKKQNGKTEREKLQKLKEIFKKIHDLKDKKE 154
 |||:||||:|
 DB 93 QICMTLASFADIGDIVGRDLYLGNPQEXXXXXX-----XXXXXXXXXXXXX 143
 QY 155 AOKRYNGEDENFYLRREDWMTANRETYWGAMTCSKEILDNSYPFATCNDTGQGPSQTHN 214
 |||:||||:|
 DB 144 XXXXXXXXNDPEFFKLREDWMTANRETYWKAITCN--XXXXXXXXXXC----- 189
 QY 215 KCRCDKDGANKGKAGGQDVTIPTYFDVYPOYLRFEEAEDPCRRKKKKLEMLEKQ 274
 |||:||||:|
 DB 190 -----XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 241
 QY 275 C-RGDKSDERYCVRNGDYCEQOTISRKGKVMGKCTDCEPACGSYENMIDNQRK 329
 |||:||||:|
 DB 242 CXXXXXXXKXXXXXKXXXXXXXKXXXXXXXKXXXXXXXKXXXXXXXKXXXXXXXK 297

RESULT 6
 US-09-924-154-14
 ; Sequence 14, Application US/09924154
 ; Patent No. US20020127241A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Narm, David L.
 ; APPLICANT: Sim, Kim L.
 ; TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use
 ; FILE REFERENCE: 05213-0465 43170-262105
 ; CURRENT APPLICATION NUMBER: US/09/924,154
 ; CURRENT FILING DATE: 2001-08-07
 ; PRIOR APPLICATION NUMBER: US 60/223,525
 ; PRIOR FILING DATE: 2000-08-07
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 1143
 ; TYPE: PRT
 ; ORGANISM: Mammalian
 US-09-924-154-14

Query Match 16.4%; Score 308.5; DB 3; Length 1143;
 Best Local Similarity 25.5%; Pred. No. 1.1e-17;
 Matches 89; Conservative 50; Mismatches 87; Indels 123; Gaps 16;

QY 9 NDVD---RFSYKEQAGY-----DNKKMKCSNGM-----TCAPFRRLHLCNKNFNNM 52
 |||:||||:|
 DB 444 NDVDIASQINVNDLRGFCGNYSNNKSWNCTGTFTNKPOTCEPPRRQTLCLGRITYLLH 503
 |||:||||:|
 QY 53 SNDSSKAKHDLAEVCAAAAYEGESIKTHYPKYDSKYPGSDPMTMLARSFADIGDIIR 112
 |||:||||:|

DB 504 RGHEDEYKEHLG---ASIEAQLKYKKEKDN-----ALCSTIIONSYADLADITIK 553
 QY 113 GRDLYLGNKKKKQNGKTEREKLQKLKEIFKKIHDLKDKKQKRYNGEDENFYLRRE 172
 |||:||||:|
 DB 554 GSDII-----KQYGGKMEENLNKYNK---DKKRNEBSLKITF-----RE 589
 QY 173 DWTANRETYWGAMTCSKEILDNSYPFATCNDTGQGPSQTHNCRCKDKGANKGKFRAG 232
 |||:||||:|
 DB 590 KMWDEKENVKVM--SAVLN-----KETCK-----DYDK----- 618
 QY 233 DGDVTIPTYFDVYPOYLRFEEAEDPCRRKKKKL---ENLEKQKQKSDERYCSR 289
 |||:||||:|
 DB 619 -----FQKLPQFLRMFKEMGDDPCERKKEKITYSFSFKVECKKD-----CDE 661
 QY 290 NGYDCEQOTISRKGKVRMGKCTDCEPACGSYENMIDNQRKQFDKQ-KKY 337
 |||:||||:|
 DB 662 N-----TCNNKCSYKKWIDLKSEYKQVQKY 689

RESULT 7
 US-10-677-980-2
 ; Sequence 2, Application US/10677980
 ; Publication No. US20050239730A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mayer, D.C.Ghislaine
 ; APPLICANT: Miller, Louis H.
 ; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE
 ; TITLE OF INVENTION: BINDING PROTEIN BASEL FOR USE AS A VACCINE
 ; FILE REFERENCE: NIH209,001C1
 ; CURRENT APPLICATION NUMBER: US/10/677,980
 ; CURRENT FILING DATE: 2003-10-02
 ; PRIOR APPLICATION NUMBER: PCT/US02/10071
 ; PRIOR FILING DATE: 2002-03-29
 ; PRIOR APPLICATION NUMBER: US 60/281130
 ; PRIOR FILING DATE: 2001-04-02
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1210
 ; TYPE: PRT
 ; ORGANISM: Plasmodium falciparum
 US-10-677-980-2

Query Match 16.4%; Score 308.5; DB 5; Length 1210;
 Best Local Similarity 25.5%; Pred. No. 1.2e-17;
 Matches 89; Conservative 50; Mismatches 87; Indels 123; Gaps 16;

QY 9 NDVD---RFSYKEQAGY-----DNKKMKCSNGM-----TCAPFRRLHLCNKNFNNM 52
 |||:||||:|
 DB 438 NDVDIASQINVNDLRGFCGNYSNNKSWNCTGTFTNKPOTCEPPRRQTLCLGRITYLLH 497
 |||:||||:|
 QY 53 SNDSSKAKHDLAEVCAAAAYEGESIKTHYPKYDSKYPGSDPMTMLARSFADIGDIIR 112
 |||:||||:|
 DB 498 RGHEDEYKEHLG---ASIEAQLKYKKEKDN-----ALCSTIIONSYADLADITIK 547
 QY 113 GRDLYLGNKKKKQNGKTEREKLQKLKEIFKKIHDLKDKKQKRYNGEDENFYLRRE 172
 |||:||||:|
 DB 548 GSDII-----KQYGGKMEENLNKYNK---DKKRNEBSLKITF-----RE 583
 QY 173 DWTANRETYWGAMTCSKEILDNSYPFATCNDTGQGPSQTHNCRCKDKGANKGKFRAG 232
 |||:||||:|
 DB 584 KMWDEKENVKVM--SAVLN-----KETCK-----DYDK----- 612
 QY 233 DGDVTIPTYFDVYPOYLRFEEAEDPCRRKKKKL---ENLEKQKQKSDERYCSR 289
 |||:||||:|
 DB 613 -----FQKLPQFLRMFKEMGDDPCERKKEKITYSFSFKVECKKD-----CDE 655
 QY 290 NGYDCEQOTISRKGKVRMGKCTDCEPACGSYENMIDNQRKQFDKQ-KKY 337
 |||:||||:|
 DB 656 N-----TCNNKCSYKKWIDLKSEYKQVQKY 683

RESULT 8

US-10-153-273-4
; Sequence 4, Application US/10153273
; Publication No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
Chilnits, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-153-273-4
Query Match 14.9%; Score 281; DB 4; Length 1435;
Best Local Similarity 23.1%; Pred. No. 3.8e-15;
Matches 78; Conservative 44; Mismatches 101; Indels 114; Gaps 10;
QY 10 DVDRFSV---KEQAGYNNKKKCSNGM-----TCAPPRRLHLCNKPNNNSNDSSKA 59
DB 453 DLDPSKFGCDKNSVDYTWKVECKNPYLSTFKDVCPPRRQELDIGNIDRIYDKLMI 512
QY 60 KHDLLAEVCMAMKAYGESIKTHYPKYDSKPSDPMCTMLARSPADIGDIIIRGDLVIG 119
DB 513 KEHILA---IAIYSRIILKRYKKRDKD-----EVCKIINKTPADIRDIIGGTDYV-- 560
QY 120 NKKKKQNGKETEREKLEQKLKEIIPKKIHNLKDKKQAKYNGDDEPNFYKLREDMWTANR 179
DB 561 -----NDLSNRLVGVKINTNSKYVHRKNKNDKL-----FDEDMWKYIK 598
QY 180 EYVWGMATCSKELNDSYFRATCNDTGQSPSOTNAKCRCDKXGANAGKPKAGDGDVTV 239
DB 599 KDVNVVI-----SWVFK-----DKTVCKEDDIBN----- 622
QY 240 PTFYFVYVQYLWFEWMAADFCKRKKKKLENLKQCRGDKSDDEVRYCSRNGYDCEQTIS 299

DB 623 -----IPQFRFMSWEGDDYCCDXTKMTIELTKVCKCKPCEDD----- 660
QY 300 RKGAVRMGKGCTDCFPAGCSYENWIDNRKQFDDQKK 336
DB 661 -----NCKSKCNSTYKEMISKKEEYNRQAK 685
RESULT 9
US-10-153-273-6
; Sequence 6, Application US/10153273
; Publication No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
Chilnits, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 749 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-153-273-6
Query Match 14.9%; Score 280.5; DB 4; Length 749;
Best Local Similarity 24.8%; Pred. No. 1.9e-15;
Matches 80; Conservative 42; Mismatches 90; Indels 111; Gaps 14;
QY 22 YDNKKMKCSNGMTAPFRRLHLC-NKNPPNNNSNDSSKAKIDLAEVCMAMKAYGESIKT 80
DB 128 YSNKVTPEGV-CGPPRRQQLCGIYFLIRDGNBEGKDH-----INKAANYEAMHLKE 181
QY 81 HYPKYDSKPSDPMCTMLARSPADIGDIIIRGDLVIGNKKKKQNGKETEREKLEQKLK 140
DB 182 KY-----ENAGGD-KICNALIGSYADIGDIVRGDVM-----RDINTNKLSEKQ 225

```

RESULT 10
US-09-924-154-15
; Sequence 15, Application US/09924154
; Patent No. US20020127241A1
; GENERAL INFORMATION:
; APPLICANT: Narum, David L.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use
; FILE REFERENCES: 05213-0465 43170-262105
; CURRENT APPLICATION NUMBER: US/09/924,154
; PRIORITY FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,525
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1086
; TYPE: prt
; ORGANISM: Mammalian
US-09-924-154-15

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RESULT 11
US-10-293-913A-4
; Sequence 4, Application US/10293913A
; Publication No. US20040022805A1
; GENERAL INFORMATION:
; APPLICANT: Natum, David

```

Qy	10	DVDFSYVEQAGYD-----	-----NKKKCSNGMTCAFPRLHLCTNKKFPMNNSDS	56
Db	309	DLDDPFS---	KFGCDKNQVDITWTKWECKPKYKSTKVCVCPRRQBECLGIDRIDRYDKL	365
Qy	57	SKAGHDLLAEVCMAAKYEGESIKTHYPKYSGSPGSPMCTMLARSPADIGDIIRGRDL	116	
Db	366	LMIEHHLLA--TATYESRLTKKKYKNKDK--	EVKTIQKTFADRIDRIIGGTDY	415
Qy	117	YLGNKKKKKQNGKETERETLEBKLEIFKTIIDNLKDXEAKQRYNGDEDPNFYKLRIDPWT	176	
Db	416	W-----	NDSLNRKLYGKITMNSYVHRN--KQNDLFLF-----RDEWK	451
Qy	177	ANRETVGAMTCSKELDNSSYFRATCNDTGGSPGQTHNKKCDYDKGANAAGKPPAAGDSG	236	
Db	452	VTKDVMNVLI-----	SWVFK-----DKTYCKEKEDIIEN-----	478
Qy	237	TIIVETPDYVQYLRFVFEEMAEDECRKKKKKLTLELKQCRCKDKSDERYVCSRNGYDEQ	296	
Db	479	-----	LPQFRFVSEWGDGDDCODTXXMIETLTKVECKEKEPCEDD-----	516
Qy	297	TISRKGVRMGKGTDCFPAGCSYENNITDNRKOFDQKKK	336	
Db	517	-----	NCRRKNSITKEMISKKKEEYNNQAK	541

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RESULT 12
US-10-293-913A-2
Sequence 2, Application US/10293913A
Publication No. US20040022805A1
GENERAL INFORMATION:
APPLICANT: Narum, David
APPLICANT: Liang, Hong
APPLICANT: Fuhrmann, Steve
APPLICANT: Sim, B. Kim lee
TITLE OF INVENTION: Synthetic Genes for Malarial Proteins and Methods of Use
FILE REFERENCE: 05213-0466 (43170-280206)
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/345,051
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 616
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic EBA-175 RII
US-10-293-913A-2

```

Query Match 14.3%; Score 269; DB 4; Length 616;
Best Local Similarity 23.2%; Pred. No. 1.5e-14;
Matches 79; Conservative 43; Mismatches 98; Indels 120; Gaps 11;

QY 10 DVDRFSVKEQAGYD-----NKKMKCSNGMTCAPFRLHLCKNKPMMNSNDS 56
DB 309 DLDDFS--KFGCDKNSVDITNTKWECKPYKLTSDVCVPRROELCLGNIDRIYDNL 365
QY 57 SKAHDLLAEVCMATKYGESIKTHYPKYDSKYGSDPMPCTMLARSPADIGDIIRGRDL 116
DB 366 LMIKEHILA---IAIYRSRLTKRKYKNKDK-----EVCKIKTKTFADIRDIIGTDY 415
QY 117 YLGNKKKKQKNGKETEREKLQKLEIFPKIHDNLKDKAQRKRYNGDEDPNFYKLRDPMWT 176
DB 416 W-----NDLSNRKLVGKINTNSNYVHRN--KQNDLTF-----RDEWKK 451
QY 177 ANRETWGAMTCSKELDNSSYFRATCNDTGQPSQTHNKKCRCDKKGANACKPKAGDGDV 236
DB 452 VIKKDVWVI-----SWVFK-----DKTVCKEDDIEN----- 478
QY 237 TIVPTFYDYVPOYLRFPEMAEDPCKKKKLEMLEKCRGKDKSDERYCSRNGYDCEQ 296
DB 479 -----IPQFRWFSEMGDDYCYQDKTKMIETLKVECKEPCBEDD----- 516
QY 297 TISRKGKVRMGKGTDCFPFACSGYENWIDNQRKQFDKQK 336
DB 517 -----NCKRKNSYKEMISKKEBYNNQAK 541

RESULT 13
US-09-924-154-13
Sequence 13, Application US/09924154
Patent No. US20020127241A1
GENERAL INFORMATION:
APPLICANT: Natum, David L.
APPLICANT: Sim, Kim L.
TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use
FILE REFERENCE: 05213-0465 43170-262105
CURRENT APPLICATION NUMBER: US/09/924.154
CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 60/223,525
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 1421
TYPE: PRT
ORGANISM: Mammalian
US-09-924-154-13

Query Match 14.3%; Score 269; DB 3; Length 1421;
Best Local Similarity 23.2%; Pred. No. 4.2e-14;
Matches 79; Conservative 43; Mismatches 98; Indels 120; Gaps 11;

QY 10 DVDRFSVKEQAGYD-----NKKMKCSNGMTCAPFRLHLCKNKPMMNSNDS 56
DB 453 DLDDFS--KFGCDKNSVDITNTKWECKPYKLTSDVCVPRROELCLGNIDRIYDNL 509
QY 57 SKAHDLLAEVCMATKYGESIKTHYPKYDSKYGSDPMPCTMLARSPADIGDIIRGRDL 116
DB 510 LMIKEHILA---IAIYRSRLTKRKYKNKDK-----EVCKIKTKTFADIRDIIGTDY 559
QY 117 YLGNKKKKQKNGKETEREKLQKLEIFPKIHDNLKDKAQRKRYNGDEDPNFYKLRDPMWT 176
DB 560 W-----NDLSNRKLVGKINTNSNYVHRN--KQNDLTF-----RDEWKK 595
QY 177 ANRETWGAMTCSKELDNSSYFRATCNDTGQPSQTHNKKCRCDKKGANACKPKAGDGDV 236
DB 596 VIKKDVWVI-----SWVFK-----DKTVCKEDDIEN----- 622
QY 237 TIVPTFYDYVPOYLRFPEMAEDPCKKKKLEMLEKCRGKDKSDERYCSRNGYDCEQ 296
DB 623 -----IPQFRWFSEMGDDYCYQDKTKMIETLKVECKEPCBEDD----- 660

QY 297 TISRKGKVRMGKGTDCFPFACSGYENWIDNQRKQFDKQK 336
DB 661 -----NCKRKNSYKEMISKKEBYNNQAK 685

RESULT 14
US-10-153-273-8
Sequence 8, Application US/10153273
Publication No. US20020169305A1
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-153-273-8

Query Match 12.8%; Score 241; DB 4; Length 921;
Best Local Similarity 26.1%; Pred. No. 6.7e-12;
Matches 84; Conservative 43; Mismatches 119; Indels 76; Gaps 17;

QY 23 DNKKMKCSNGMTCAPFRLHLCKNKPMMNSNDSKAKHDLLAEVCMATKYGESIKTHY 82
DB 427 DESKIKMGOGAGCIPRRORKLCTHYLEKIMTN-TNELKYAFIK--CAA--ETPLWQNY 481
QY 83 PK-----YDSKYGSDP--MCTMLARSPADIGDIIRGRDYLGNKKKKQKNGKETER 132
DB 482 KQDKNGAEDLDEKLGKGIIPEDFKROMFYTFADIRDICGTDI-----SSKQTSKGV-- 535
QY 133 EKLQKLEIFPKIHDNLKDKAQRKRYNGDEDPNFYKLRDPMWTANRETWGAMTCSKEL 192
DB 133 -----IPQFRWFSEMGDDYCYQDKTKMIETLKVECKEPCBEDD----- 660

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Db      536  GKVCNCINDVEFYKXSNISI-----RY-----RKSMWETNGPVIWEGMLCALSY 577r
Oy      193  DNSSYFRPATCNDTDTGQSPSTQTHAKCRCDDKGNAGKPAAGDGYTYPTTYDYIPQTLRW 252r
Db      578  DTG-----LNNYNN-----PETHKKL-----TEGNNNEFEKYIFGSDSTSLTSKFSERPOELRW 624r
Oy      253  FEEMAEEDFCRKKKKKKLEMLEKQCRGKDSDRYRYSRNGYCEQTLISRKGVWRMGKCTD 312r
Db      625  LTWEGNEFPCRQKKEKKEVKVLLAKCK-----PCD--VDGDKCN-GK-CVA 664r
Oy      313  CFPACGSYEN-----WIDNORKQ 330r
Db      665  CKDQCKQYHSHWIGIWIWIDNYKKQ 686r

```

RESULT 15

US-09-924-154-16
 Sequence 16, Application US/09924154
 Patent No. US20020127241A1
 GENERAL INFORMATION:
 APPLICANT: Narum, David L.
 APPLICANT: Sim, Kim L.
 TITLE OF INVENTION: Anti-plasmodium Compositions and Methods of Use
 FILE REFERENCE: 05213-0465 43170-262105
 CURRENT APPLICATION NUMBER: US/09/924,154
 CURRENT FILING DATE: 2001-08-07
 PRIOR APPLICATION NUMBER: US 60/223,525
 PRIOR FILING DATE: 2000-08-07
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 16
 LENGTH: 972
 TYPE: PRT
 ORGANISM: Mammalian
 US-09-924-154-16

Query Match	12.5%;	Score 235;	DB 3;	Length 972;
Best Local Similarity	25.3%;	Pred. No. 2.4e-11;		
Matches	88;	Conservative	40;	Mismatches 114;
				Indels 106;
				Gaps 16;

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QY      2 KKKQKGGDVDBFSVYKQAGYDNKKKKGNGM-----TCAPRRRLHLNKNFEN---NM 52
Db      138 CEE--KGND-----KWCQCNNEHIKDFPDVCGPERRQOLCLGNLDKQEFKN 181

QY      53 SNDSKAKHDLAEVQMAKYEGESIKTYPK--YDSKYPGSDPFWCTMLARSFADIGDI 110
Db      182 VNDLKK-----FLNEIILGIRDECKFLIEKRRKMHENMY--LDERACKYLTNYSFDDYKNI 235

QY      111 IGRGDLVYGNKKKKQNGKETEKEBKEQKLKEIFKKIHDNLKQKQAKRYNGDEDPNFYKL 170
Db      236 ILGKQMW-----RDPNSIKTENILKGNBEGIKANI-----VSMVSYADLSIDEF 280

QY      171 REDMWTANSETYWGAMTCSKELDNSSYPFATCNDIQGSGSQTHNKKRCQDKKAKANAGKPK 230
Db      281 RGHMWDQNKQJLMEALISC-----EPYGG--NHTG-----VCLIMEDND----- 316

QY      231 AGDGDVITVPTFYFDVYPOYLWFEWEAEDEPCKRKKKKLLENLEKQCRGKQKSDSDRYRCSRN 250
Db      317 -----NOYLHMERKKNDFCIDKLNMNDVIKPC--IDKRVKSPKRSN 358

QY      291 GYDCQGLTSRKKGKVMKMGKQCTDQCFAGSGSYENMIDNORKQFDRQ--KKY 337
Db      359 PSDV-----ATVGNKSCCTDIDKMIINRRKREYKQSSKTY 391

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Search completed: December 29, 2005, 23:40:13
Job time : 38.7534 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 23:15:22 / Search time 2.14866 Seconds

(without alignments)
1174.559 Million cell updates/sec

Title: US-09-508-967-1_COPY_79_415

Perfect score: 1884

Sequence: 1 PCKKDGKGNVDPRFSVKEQA.....GSYENWIDNRKQFDKQKKY 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEM_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEM_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEM_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEM_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	5.4	1142	US-11-109-156-22	Sequence 22, Appli
2	98	5.2	454	US-11-089-551A-35	Sequence 35, Appl
3	93.5	5.0	1238	US-11-078-735-21	Sequence 21, Appl
4	89.5	4.8	436	US-10-131-826A-404	Sequence 404, App
5	85.5	4.5	369	US-11-078-735-38	Sequence 38, Appl
6	85.5	4.5	484	US-11-078-735-43	Sequence 43, Appl
7	85.5	4.5	558	US-10-512-109-11	Sequence 11, Appl
8	85.5	4.5	723	US-10-131-826A-346	Sequence 346, App
9	85.5	4.5	723	US-11-078-735-17	Sequence 17, Appl
10	82	4.4	557	US-10-512-109-9	Sequence 9, Appl
11	82	4.4	646	US-10-491-096-190	Sequence 190, App
12	82	4.4	785	US-11-109-157A-5	Sequence 5, Appl
13	82	4.4	1076	US-11-109-157A-5	Sequence 25, Appl
14	82	4.4	1907	US-11-039-398-25	Sequence 25, Appl
15	82	4.4	4655	US-10-995-561-556	Sequence 556, App
16	81.5	4.3	322	US-11-073-605-4	Sequence 4, Appl
17	81.5	4.3	364	US-10-131-826A-186	Sequence 186, App
18	81.5	4.3	370	US-11-073-605-2	Sequence 2, Appl
19	81.5	4.3	370	US-11-075-400-14	Sequence 14, Appl
20	81.5	4.3	2004	US-10-467-657-84	Sequence 84, Appl
21	81.5	4.3	2004	US-10-467-657-84	Sequence 6342, Ap
22	81	4.3	654	US-10-770-726-82	Sequence 82, Appl
23	80.5	4.3	468	US-10-131-826A-90	Sequence 90, Appl
24	80.5	4.3	468	US-11-102-240-150	Sequence 150, App
25	80	4.2	531	US-11-060-914-4	Sequence 4, Appl

26	79.5	4.2	963	US-10-467-962B-2	Sequence 2, Appli
27	79.5	4.2	1976	US-11-069-834-52	Sequence 52, Appl
28	79.5	4.2	2897	US-10-499-715-2	Sequence 2, Appl
29	79	4.2	208	US-10-793-626-694	Sequence 694, App
30	79	4.2	208	US-10-793-626-1326	Sequence 1326, Ap
31	79	4.2	331	US-11-078-735-33	Sequence 33, Appl
32	79	4.2	332	US-11-078-735-51	Sequence 51, Appl
33	79	4.2	402	US-10-485-517-422	Sequence 422, App
34	78.5	4.2	1218	US-11-078-735-20	Sequence 20, Appl
35	78	4.1	2515	US-11-113-424-53	Sequence 53, Appl
36	77	4.1	315	US-10-878-556A-178	Sequence 178, App
37	77	4.1	333	US-10-821-234-1036	Sequence 1036, Ap
38	76.5	4.1	667	US-10-821-234-1477	Sequence 1477, Ap
39	76.5	4.1	693	US-10-873-528-185	Sequence 185, App
40	76	4.0	989	US-10-793-626-2594	Sequence 2594, Ap
41	76	4.0	2214	US-11-080-991-54	Sequence 94, Appl
42	75.5	4.0	1976	US-11-069-834-54	Sequence 54, Appl
43	75.5	4.0	472	US-10-793-626-1902	Sequence 1902, Ap
44	74.5	4.0	655	US-10-793-626-1052	Sequence 1052, Ap
45	74.5	4.0	655	US-10-793-626-1400	Sequence 1400, Ap

ALIGNMENTS

RESULT 1
US-11-109-156-22
Sequence 22, Application US/11109156
Publication No. US20050250144A1
GENERAL INFORMATION:
APPLICANT: Toshio Ota
APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
APPLICANT: Koji Hayashi
APPLICANT: Kaoru Otsuka
APPLICANT: Jun-ichi Yamamoto
APPLICANT: Shizuko Ishii
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Ai Wakamatsu
APPLICANT: Keiichi Nagai
APPLICANT: Tetsuji Otsuki
APPLICANT: Shin-ichi Funahashi
APPLICANT: Chiaki Senoo
APPLICANT: Jun-ichi Nezu
TITLE OR INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
TITLE OR INVENTION: PHOSPHATASE
FILE REFERENCE: 06501-099002
CURRENT APPLICATION NUMBER: US/11/109,156
CURRENT FILING DATE: 2005-04-19
PRIOR APPLICATION NUMBER: US/10/060,065
PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JP00/05061
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: JP 11-248036
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 1142
TYPE: PRT
ORGANISM: Homo sapiens
US-11-109-156-22

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Query Match      5.4%; Score 101; DB 7; Length 1142;
Best Local Similarity 22.9%; Pred. No. 0.67;
Matches 81; Conservative 40; Mismatches 74; Indels 158; Gaps 25;

QY 24 NKKKCSNGMTCCAPRRRLHLCN-----KNFPNNMSNSKAKHDLAIVCMAYEG-- 75
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 214 NKSIRORRLT-----RRINNVPKDLKEFNKTKTCOSSVSTHDL-----KXYRLATL 262
QY 76 ESIKTHYPKSDSKYPSDFPMTMLAR3FA-----DIGDILRGRLYLGK-----K 122
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 263 ETLTGHY-----GALIFETSMLLISENEMMFHSDGNVLYEVMTGNLGIOWR 314
QY 123 KKQNGKTEREKLBOKLKIFPKIHDLKDXEAQRRYNGDEDPFYKJREDPMWTAN---- 178
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 315 HKPNVSVYKERE--NKLKR--KQLEN--KDKX-----DESKN--KIREMNNSFFPE 359
QY 179 -----RETWGAMTCSKELDN-----SSYFRAT-----CNDT 205
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 360 ITHIVIKESV---VSINKQ-DNKKMELKLSHEBALSFVSLVDGFRLTADAHYLCIDV 415
QY 206 G-----OGPSOTH--NKCRCDDKGANAGPKAGDGVITVTFYFDVYPOYL 250
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 416 APPLVHNIGONGCHPCTEYAINLKR--QBSSEGM-----YV---L 453
QY 251 RPFEBWADF-----CRKKKKLLENLEKQCR-----GDKDS 281
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 454 RMS---CTDFDNILMTVTCFEKSEBOVQAKQKFKQIEVQKGRYSLHSDRS 503

RESULT 2
US-11-089-551A-35
; Sequence 35, Application US/11089551A
; Publication No. US20050266242A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al.
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40025A
; CURRENT FILING DATE: 2005-03-24
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US 60/559,286
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-089-551A-35

Query Match      5.2%; Score 98; DB 7; Length 454;
Best Local Similarity 20.2%; Pred. No. 0.4;
Matches 72; Conservative 35; Mismatches 128; Indels 122; Gaps 17;

QY 3 KKKQKGNVDFRS---YKEQAGYNNKKMGKCSNGMTCCAPRRRLHLCNCFPMANSN---- 54
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 57 KATDPAADTKYXSNDKSKRSANSNDKDC-----RTTNDMTTRYDSKRYT 104
QY 55 --DSSKAGHDLAIVCMAYEGES1-KTHYPKYDSKYPGSDPMTMLAR3FADIGDI 111
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 105 NCDHKAASHSM-----KTKKRSVDKDHMKDSSYKAS-----KNSHNYST--NTM 149
QY 112 RGRDLY---LGNKKKQNGKTEREKLBOKLKIFPKIHDLKDXEAQRYNGDEDPNF 167
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 150 NKMDVYTKANMANKKK-----SDTSTWKKKNSHVSYN-----NDKSKTKMYNDSDDDD 199
QY 168 YKLREDMTATARETYGAMTCSKELDNSSYFRATNDTGOQPSQTHN-----KCR 217
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 200 NNVNNDNNNN-----NKNDNNNDNNNDTSNNNNNNNNRKNRNNRDMWTXKCT 249
QY 218 CDKQGANAGPKAGDGVITVTFYFDVYPOYLRFEBWADFCKKKKKLENLEKQCRG 277
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 250 DMNDKRDNNNK-----NDMANNDNKYNNNNVKKR--- 277

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QY 278 KDKSDERYCSRNGYDEBQT-----SRKGVRMGKCTDCCFACSYENMIDNQR 329
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 278 NHKSS---CRIDGYSANNAVNASTHASNKNVNDMMN-----DTYKNKTDNKK 321

RESULT 3
US-11-078-735-21
; Sequence 21, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAM JAMES
; APPLICANT: TUDAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-21

Query Match      5.0%; Score 93.5; DB 7; Length 1238;
Best Local Similarity 19.9%; Pred. No. 3.1;
Matches 39; Conservative 25; Mismatches 65; Indels 67; Gaps 9;

QY 175 WTANRETVWGMATMSKELD-----NSSYFRATCNTDGOQPSQTHNKKR 217
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 291 WQNCETNWGGLCDKDLNCGSHHPCTNGTCTINAEPPDYRCTCPGYSGRN----- 343
QY 218 CDKQGANAGPKAGDGVITVTFYFDVYPOYLRF-----FEBWADFCKKKKKL 268
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 344 CEKREHACTSNPCANGSGCHEVPSGFECRCS--GNSGPTCALDIDCASNPCAAAGTGV 401
QY 269 ENLE-----KQCRGKDKSDERY-----YC---SRNGYDEBQT 297
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 402 DQVQGFRCITCEQWVGATCOLDANECGKCLNLFSCKNLIGYCDICIPGMKINGCHIN 461
QY 298 ISR-KKVRMGKCTD 312
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 462 VNDRCGQCHGGTCKD 477

RESULT 4
US-10-131-826A-404
; Sequence 404, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Deenoysers, Luc

```

	Query Match	4.8%	Score 89.5;	DB 6;	Length 436;
	Best Local Similarity	18.8%	Pred. No. 1.9;		
	Matches	66;	Conservative	48;	Mismatches 136; Indels 101; Gaps 15
Qy	18	EQAQYDNKKMKCSNGMTCAFFRRRLHLCNKNFNM--NSNDSSKAKHDLLAEVCAAYKE	74		
Db	122	KAAVDTHQWMPILSTCKQ-----CPVVYVSPOGSDGHHTYSPQCKLEYDACYLGKD I	175		
Qy	75	GESITTHYPKIDSKTPGSDPFMCPTMLAASFADIGIIRGRDLYLGNKKKKKGKNGKETERPK	134		
Db	176	SVKCEGHCP-----CPSDKPRTST-----SRNVKRCASDLFERE	208		
Qy	135	LEOQLKEJLFPKKIH D--NLKHDEAKQRNGEDENPNFYKLARE D--MWTANR-AETWAGAMT	187		
Db	209	VANRLRDPMFKALHESGSQNKTKYTLLRPERSFTDSLPTCDOSJGMNFNRLDYTDLL-	267		
Qy	188	CSKELDNSSYFRATCNTDTGGQSQTTHNCRCSCKDGANAAGKPKAGGDVTIVPTFDVP	247		
Db	268	----LDGEELRSIYLDKNEQCRTKAFNSDITYKDS-----	298		
Qy	248	QYLRFEEWAEDFCRK---KKKLENIEKQCGXKSDSEY-RYSRNGY---DCEQT- 297			
Db	299	--LIENNWCYCFOQODPPCQTELSNIQKRQGVKKLLGOUYPLDCDEDYYUKPTQCHGSV	356		
Qy	298	-----ISRKGRVRMG-----KGCYDFC-----FACGSVENMIIDNQKQFD 332			
Db	357	QQCWCVDRYGNEWGSRIINGVADCAIDFEISGFDFASGGDFHEWTTDEBDDDD 407			

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Query Match          4.5%; Score 85.5; DB 7; Length 369;
Best Local Similarity 28.6%; Pred. No. 3.4;
Matches      20; Conservative    10; Mismatches     23; Indels   17; Gaps    3

Oy      175 WTANRETYGAMTCSKEIDNSSYFR-----ATCNDTGOG-----PSQTHNKC-----R 217
        ||| | :|| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db       272 WQCNCQEGMGLFCPCNDLNTCYCTHHKPCKNAGACTMTGGSGSYSCRCRPYTGTATCELGLIDE 311
        ||| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Oy      218 CDKDKGANAG 227
        ||| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db       332 CDPSPCKNGG 341

RESULT 6
US-11-078-735-43
; Sequence 43, Application US/11078735
; Publication No. US20050261477A1

GENERAL INFORMATION:
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: MCKENZIE, GRAHAME JAMES
APPLICANT: TUGAL, TANARA

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS

FILE REFERENCE: 674525-2019
CURRENT APPLICATION NUMBER: US/11/078,735
CURRENT FILING DATE: 2005-03-10
PRIOR APPLICATION NUMBER: PCT/GB03/03908
PRIOR FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: PCT/GB03/03285

```

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; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 43
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-078-735-43

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Query Match          4.5%; Score 85.5; DB 7; Length 484;
Best Local Similarity 28.6%; Pred. No. 4.6;
Matches 20; Conservative 10; Mismatches 23; Indels 17; Gaps 3;

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QY 175 WTANRETVGAMTCKEIDNSYFR-----ATCNDTGG-----PSQTHNK-----R 217
DB 272 WQNCQBEWGGILFCNQDLYNCTHHKPCXGATCTNTGGSYTSCRPYGTATCELGIDE 331
QY 218 CDKXGKANAG 227
DB 332 CDPSPCKXNG 341

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RESULT 7
US-10-512-109-11
; Sequence 11, Application US/10512109
; Publication No. US20050255546A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: POLYPEPTIDE HAVING AN ACTIVITY TO SUPPORT PROLIFERATION OR SURVIV
; TITLE OF INVENTION: OF HEMATOPOIETIC STEM CELL OR HEMATOPOIETIC PROGENITOR CELL, AND
; FILE REFERENCE: 905W010P1572
; CURRENT APPLICATION NUMBER: US/10/512,109
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/376,001
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-512-109-11

```

```

Query Match          4.5%; Score 85.5; DB 6; Length 558;
Best Local Similarity 24.1%; Pred. No. 5.5;
Matches 45; Conservative 32; Mismatches 63; Indels 47; Gaps 11;

```

```

QY 14 PSVKE--QAGYNKKMK--CSNGMTCAPR--RIHLCKNKPNNNS--NDSXKXKHDLLAEV 67
DB 44 FLSLVPPQAEISGEHLRCPGGYTCTSEMEENLNRSIALETALRUSSRYLQMLAT- 102
QY 68 CMAAYEGESIKTHYPKY--DSK-----YPSGDPFPMCTMLARSPADIGDI--RGRD 115
DB 103 -----QARSPFDHQHLNDSERTLQATFPGAFGEIYTONARARLDLYSEKRLYYRGAN 156
QY 116 IYLGKXKKKXKNGKTEREKLEQKLEIFKKIHNT-----KXEAQKRYNGDD 164

```

```

DB 157 LHL-----BETLAEPWALIERLFCQULHPOLLPPDYLDCLGQKQAEALRPF--EA 205
QY 165 PNFYKLR 171
DB 206 PRELRLR 212

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RESULT 8
US-10-131-826A-346
; Sequence 346, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-346

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Query Match          4.5%; Score 85.5; DB 6; Length 723;
Best Local Similarity 28.6%; Pred. No. 7.4;
Matches 20; Conservative 10; Mismatches 23; Indels 17; Gaps 3;

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QY 175 WTANRETVGAMTCKEIDNSYFR-----ATCNDTGG-----PSQTHNK-----R 217
DB 272 WQNCQBEWGGILFCNQDLYNCTHHKPCXGATCTNTGGSYTSCRPYGTATCELGIDE 331
QY 218 CDKXGKANAG 227
DB 332 CDPSPCKXNG 341

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RESULT 9
US-11-078-735-17
; Sequence 17, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAM JAMES
; APPLICANT: TUGAL, TANARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT FILING DATE: 2005-03-10
; PRIOR FILING DATE: 2003-09-09
; PRIOR FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 17
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-17

Query Match          4.5%; Score 85.5; DB 7; Length 723;
Best Local Similarity 28.6%; Pred. No. 7.4;
Matches 20; Conservative 10; Mismatches 23; Indels 17; Gaps 3;

QY 175 WTANRETYWAMTSCKEIDNSSYFR-----ATCNDTGG-----PSQTNKC-----R 217
DB 272 WQCNCOBEGWGLFCNQDINCYCTHHKPCKNKATCTWTGQSYTCSGCRPGYATCELGIDE 331
QY 218 CDKXKGANAG 227
DB 332 CDSPCKNGG 341

RESULT 10
US-10-512-109-9
; Sequence 9, Application US/10512109
; Publication No. US20050255546A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: POLYPEPTIDE HAVING AN ACTIVITY TO SUPPORT PROLIFERATION OR SURVIVAL
; TITLE OF INVENTION: OF HEMATOPOIETIC STEM CELL OR HEMATOPOIETIC PROGENITOR CELL, AND
; TITLE OF INVENTION: FOR THE SAME
; FILE REFERENCE: 905WOIOP1572
; CURRENT FILING DATE: 2004-10-21
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/376,001
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Mus musculus
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US-10-512-109-9

Query Match          4.4%; Score 82; DB 6; Length 557;
Best Local Similarity 24.3%; Pred. No. 11;
Matches 45; Conservative 31; Mismatches 65; Indels 44; Gaps 12;

QY 14 FSVKE--QAGYDNKKMK-CSNGMTCAFPRLHLCNKNPNNNSNDSSKAKHD--LLAEVC 68
DB 44 FSLSDVQAEISGHLHCPOGYCTCSB-----MEENLAHSMELBSALHDSRALQAT 99
QY 69 MAATYBESIKTHYPK--DSK-----YQSDPMTCTMLARSPADIGDII-----RRDL 116
DB 100 LATQHG--IDDFQRLNDSERTLOEAPFAGFDLYTQNTFRADLYVELRLYYRANTL 157
QY 117 YLGKKKKKQKQKTEREKLEOKLEIFPKIHDNL-----KQKQAQRYNGDEDPN 166
DB 158 HL-----EETLAEFMALRLERLKQHLPPDLYDCLGQKQAEALRPF-GDA-PR 206
QY 167 FYKLR 171
DB 207 ELRLR 211

RESULT 11
US-10-491-096-190
; Sequence 190, Application US/10491096
; Publication No. US20050267020A1
; GENERAL INFORMATION:
; APPLICANT: FAURE, OLIVIER
; APPLICANT: KOSMATOPOULOS, KONSTADINOS
; TITLE OF INVENTION: POLYPEPTIDES DERIVED FROM INDUCIBLE HSP70 AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS CONTAINING THE SAME
; FILE REFERENCE: 0508-1098
; CURRENT FILING DATE: 2004-03-29
; PRIOR FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10821
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: FR 01402496.2
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 190
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-491-096-190

Query Match          4.4%; Score 82; DB 6; Length 646;
Best Local Similarity 20.1%; Pred. No. 13;
Matches 80; Conservative 63; Mismatches 163; Indels 92; Gaps 19;

QY 14 FSVKEQAG-----YDNKKMKCSNGMTCAFPRLHLCNKNPNNNSNDSSKAKHDL-- 63
DB 217 FEVSTAGDTHLGGEDFDNRV-----NHFLAEFRKH-----KQDSENKRAVR 262
QY 64 LAEYCAATYBESIKTHYPKSDSKYPCGSDPEPMCTMLARSPADIGDII----- 113
DB 263 LRTACERAKRTLSSSTQASIEIDSLYEGIDFYYSITR--FEENALDFRTLDPEKAL 321
QY 114 RDLVNGKKKKKON-----GKTEREKLQKLEIF--KKIHDNLKDEKA-----QRY 159
DB 322 RDACL-DKQIHDLVAVGSTRIPKIOKLQDFNGEINKSINPDAVGAIVQAAIL 380
QY 160 NGDEDPN--FYKLREDWMTANRETYWAMTSCKEIDNSSYFRATCNDTGGQPSQTNKC 216
DB 381 SGDSBNVQDILLDDVPLSLGIETAGVMTVLIKRWTIIPKQTFQFTYSDNQGVLI 440
QY 217 RC-DKXGANAAGRKADGDVTVIPTYFDVVPQYLRFEEMA----- 257
DB 441 QVEGERAMTKDNNLLGKFELGTGIPAPRGVPLEVTFDIDANGILVSAVSTGKBNK 500
QY 258 -----EDFCRKKKKKLLENLEKQC--RGKDKSDEYRCRN-----GYDCEQTI--SRKG 302
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Qy 1 PCKDKGKNDVDRFSYKQAGYDNKKKCSNGMTCAFRRLHLCKNKPNNNSNDSSKX 60
Db 682 PCGCD--TNDICVGLCRQAGCD-----HVLN-----SKAR 710
Qy 61 HDLIAEVCMAAKYGEISTKTHYPKYDSKYPGSDPFM-----CTMLARSPADIGD--- 109
Db 711 RD-----KGVCGGNSCKTVAFTVHYGNTVVRIPAGATNIDVQHSFGSGETDDN 766
Qy 110 -----IRG-----RDLYGNKKKKQNGKET--ER---EKLEOKLKEIFK 144
Db 767 YLALSSSKGEFLNGFVVTMAKREIRIGNAVERSGSETVERINSTDRLEQEL--- 822
Qy 145 KIHNLKDKAQAQKNGDEDPNFY-----KLREDMWTANRETVGAMTSKELDNSSYFR 199
Db 823 -----LQVLSTVGLYNPVRYSFNPIEDKQGFYW--NSHGPMQA--CSKPCGGERKX 873
Qy 200 ATCNDYGGPSQTHNKKCDK-DKGANAGKPAAGDGYTVFYFDVVPQYLRF----- 253
Db 874 LVC--TRESQTLVSDQCRDLPGGHITBPCGTDCD-----LRMHTVASRS 917
Qy 254 -----BEMADPCKKKKKLEKCKRGKDKSDBYRY 286
Db 918 ECSAQCGGYRTLDIYCAKYSRLDKTEKVDVDFCSHPR-SNREK-CSGBCNTGWMRY 975
Qy 287 -----CSRNGYCEQOTISRK 301
Db 976 SAMTECKS---CDGCTQR 992

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RESULT 15

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US-10-995-561-556
; Sequence 556, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 556
; LENGTH: 4655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-556

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Query Match 4.4%; Score 82; DB 6; Length 4655;
 Best Local Similarity 20.4%; Pred. No. 1.3e+02;
 Matches 82; Conservative 41; Mismatches 130; Indels 148; Gaps 26;

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Qy 19 QAGYNKKMKCSNGMTCAFRRLHLCKNKPNNNSNDSSKXGDLIAEVCMAKYE- 74
Db 2823 QSGY---TKCHNSNICIP--RVYLCDGDNDGCDNSDENPTYCTTH-----TCSSEFQC 2871
Qy 75 --GESIKTHY--PKYDSKYPGSDPF-MC-----TMLARSP-ADIGDIIRGRDLYGNKK 123
Db 2872 ASGRICIPQHWYCDQTDPCFASDEPASCBSERTCLADEFKDGGRCIPSEWICPDGND 2931
Qy 124 KONGETEREKLEQKLKEIPKXIHNLKDKAQAQKNGDEDPNFYKLREDMWTANRETVW 183
Db 2932 GDMSEDEKXHQQ-----NONCSDBEF--LCVNDPRPDRRCIPQSW-----VCD 2973
Qy 184 GAMTSKELD-NSSYFRATCNTD-----GQG-----PSQTHNKR----- 217
Db 2974 GVDVCTDGYDENQNCCTRRCTCSENEFTCGGLCTPKIFRCDRHNDGQYSDEKGLYQTCQ 3033
Qy 218 -----CDKDKGANAGKPAAGDGYTVFYFDVVPQYLRFEMADPF 260
Db 3034 QNGFTCGNGRCISKTFVDEBDN-----DCGDSDELN--HLCHTP-----EPT 3074

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Qy 261 CRKKKKLEL-----LEKQCRG-----KDKSEYRYCSRN-----GYDCEQOTIS-- 299
Db 3075 CPPIEFKCDNGRCIEMMKLCNHLDDCLDNDSE--KGCGINECHDPSISGCHNCTDTLTSF 3133
Qy 300 -----RKGVYRMG-----KGTDCRFAC-----GSY 320
Db 3134 YCSGPGYKLMSDKRTCVIDIDECTEMPVCSQKCNENIGST 3174

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Search completed: December 29, 2005, 23:40:23
 Job time : 3.14866 secs

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